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OM protein - protein search, using sw model

Run on: March 3, 2004, 10:27:20 ; Search time 20.3333 Seconds
(without alignments)
309.756 Million cell updates/sec

Title: US-09-987-485A-1
Perfect score: 615
Sequence: 1 MKLKVTVTNGTAYDVEDVDK.....KVLVKERDAVQGGGLIKIG 122

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues
Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 20000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep.*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	615	100.0	124	US-09-364-083-2	Sequence 2, Appli
2	615	100.0	124	US-09-651-419-2	Sequence 2, Appli
3	604.5	98.3	123	US-07-956-700B-107	Sequence 107, App
4	604.5	98.3	123	US-08-476-537-107	Sequence 107, App
5	604.5	98.3	123	US-08-485-607-107	Sequence 107, App
6	604.5	98.3	123	US-08-475-879-107	Sequence 107, App
7	604.5	98.3	123	US-07-687-819-1	Sequence 1, Appli
8	604.5	98.3	123	US-09-433-043B-107	Sequence 128, App
9	598.5	97.3	123	US-09-433-043B-128	Patent No. 5252466
10	518.5	84.3	106	5252466-6	Patent No. 5252466
11	310	50.4	66	5252466-1	Sequence 2, Appli
12	211	34.3	43	US-07-687-819-2	Sequence 127, App
13	202.5	32.9	170	US-09-433-043B-127	Sequence 106, App
14	200.5	32.6	165	US-07-956-700B-106	Sequence 106, App
15	200.5	32.6	165	US-08-476-537-106	Sequence 106, App
16	200.5	32.6	165	US-08-485-607-106	Sequence 106, App
17	200.5	32.6	165	US-08-475-879-106	Sequence 106, App
18	200.5	32.6	165	US-09-433-043B-106	Patent No. 5252466
19	193.5	31.5	100	5252466-19	Sequence 6221, Ap
20	175.5	28.5	147	US-09-134-000C-6221	Sequence 19134, A
21	168.5	27.4	612	US-09-252-991A-19134	Sequence 2, Appli
22	159.5	25.9	1140	US-09-220-081-2	Sequence 2, Appli
23	159.5	25.9	1140	US-09-677-575-2	Sequence 5587, Ap
24	153	24.9	652	US-09-328-352-5587	Sequence 27999, A
25	152	24.7	701	US-09-252-991A-27999	Sequence 166, App
26	150	24.4	108	US-08-997-080-166	Sequence 166, App
27	150	24.4	108	US-08-997-362-166	Sequence 166, App

28	150	24.4	108	3	US-09-095-855-166	Sequence 166, App
29	150	24.4	108	4	US-09-324-542-166	Sequence 166, App
30	150	24.4	108	4	US-09-205-426-166	Sequence 166, App
31	150	24.4	190	4	US-09-107-532A-5720	Sequence 5720, Ap
32	150	24.4	243	3	US-09-095-855-199	Sequence 199, App
33	150	24.4	243	4	US-09-205-426-199	Sequence 199, App
34	149	24.2	1154	4	US-09-134-001C-3428	Sequence 3428, Ap
35	148.5	24.1	676	4	US-09-252-991A-26143	Sequence 26143, A
36	147	23.9	117	4	US-09-673-395A-230	Sequence 230, App
37	144	23.4	1163	4	US-09-134-000C-5707	Sequence 5707, Ap
38	139.5	22.7	168	4	US-09-134-000C-4552	Sequence 4552, Ap
39	137	22.3	67	6	5252466-5	Patent No. 5252466
40	136.5	22.2	158	1	US-08-611-107-4	Sequence 4, Appli
41	136.5	22.2	158	2	US-08-422-560A-4	Sequence 4, Appli
42	136.5	22.2	158	3	US-08-468-793-4	Sequence 4, Appli
43	133	21.6	257	1	US-07-956-700B-105	Sequence 105, App
44	133	21.6	257	1	US-08-476-537-105	Sequence 105, App
45	133	21.6	257	1	US-08-485-607-105	Sequence 105, App

ALIGNMENTS

RESULT 1
US-09-364-083-2
; Sequence 2, Application US/09364083
; Patent No. 6210676
; GENERAL INFORMATION:
; APPLICANT: Callister, Steven M
; APPLICANT: Lovrich, Steven D
; APPLICANT: Schell, Ronald F
; APPLICANT: Jobe, Dean A
; TITLE OF INVENTION: Compositions and Method Using the Borrelia burgdorferi Outer Surface
; TITLE OF INVENTION: Epitope(s) of Borrelia burgdorferi Outer Surface
; TITLE OF INVENTION: Protein C (OspC) for the Diagnosis and Prevention of
; TITLE OF INVENTION: Lyme Disease
; FILE REFERENCE: B. burgdorferi OspC
; CURRENT APPLICATION NUMBER: US/09/364,083
; CURRENT FILING DATE: 1999-07-30
; EARLIER APPLICATION NUMBER: 60/094,955
; EARLIER FILING DATE: 1998-07-31
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 2
; LENGTH: 194
; TYPE: PRT
; ORGANISM: Borrelia burgdorferi
US-09-364-083-2

Query Match	100.0%	Score 615;	DB 3;	Length 194;
Best Local Similarity	100.0%	Pred. No. 2.8e-57;		
Matches	122;	Conservative	0;	Mismatches
			0;	Indels
				Gaps
				0;

Qy	1	MKLKVTVTNGTAYDVEDVDKSHENPMGTILFGGTGGAPAPAAAGGAGAGKAGEGEIPAPL	60
Db	1	MKLKVTVTNGTAYDVEDVDKSHENPMGTILFGGTGGAPAPAAAGGAGAGKAGEGEIPAPL	60

Qy	61	AGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVKVVKERDAVQGGGLIK	120
Db	61	AGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVKVVKERDAVQGGGLIK	120

Qy	121	IG 122
Db	121	IG 122

RESULT 2
US-09-651-419-2
; Sequence 2, Application US/09651419
; Patent No. 6464985
; GENERAL INFORMATION:
; APPLICANT: Callister, Steven M
; APPLICANT: Lovrich, Steven D

```

; APPLICANT: Schell, Ronald F
; APPLICANT: Jobe, Dean A
; TITLE OF INVENTION: Compositions and Method Using the Borrelia burgdorferi Outer Surface
; TITLE OF INVENTION: Epitope(s) of Borrelia burgdorferi Outer Surface
; TITLE OF INVENTION: Protein C (OspC) for the Diagnosis and Prevention of
; TITLE OF INVENTION: Lyme Disease
; FILE REFERENCE: B. burgdorferi OSpC
; CURRENT APPLICATION NUMBER: US/09/651,419
; CURRENT FILING DATE: 2000-08-30
; PRIOR APPLICATION NUMBER: 60/094,955
; PRIOR FILING DATE: 1998-07-31
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 194
; TYPE: PRT
; ORGANISM: Borrelia burgdorferi
US-09-651-419-2

Query Match      100.0%; Score 615; DB 4; Length 194;
Best Local Similarity 100.0%; Pred. No. 2.8e-57;
Matches 122; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MKLKVTVNGTAYDVDVDVKSHENPMGTILFGGGTGGAPAPAAAGGAGAGKAGEGEIPAPL 60
Db      1 MKLKVTVNGTAYDVDVDVKSHENPMGTILFGGGTGGAPAPAAAGGAGAGKAGEGEIPAPL 60

QY      61 AGTVSKILVKEGDTVKGQTVLVLEAMKMETEINAPTDGKVEKVLVKERDAVQGGQGLIK 120
Db      61 AGTVSKILVKEGDTVKGQTVLVLEAMKMETEINAPTDGKVEKVLVKERDAVQGGQGLIK 120

QY      121 IG 122
Db      121 IG 122

RESULT 3
US-07-956-700B-107
; Sequence 107, Application US/07956700B
; Patent No. 5539092
; GENERAL INFORMATION:
; APPLICANT: Robert Haselkorn and Piotr Gornicki
; TITLE OF INVENTION: Cyanobacterial and Plant Acetyl-CoA
; TITLE OF INVENTION: Carboxylase
; NUMBER OF SEQUENCES: 116
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: 321 No. 5539092th Clark Street
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60610
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII-DOS
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/956,700B
; FILING DATE: 19921002
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Thomas E. No. 5539092thrup
; REGISTRATION NUMBER: 33,268
; REFERENCE/DOCKET NUMBER: ARCD:058
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 1-312-744-0090
; TELEFAX: 1-312-755-4489
; INFORMATION FOR SEQ ID NO: 107:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 123 amino acids
; TYPE: Amino acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; MOLECULE TYPE: Peptide
US-08-476-537-107
Query Match      98.3%; Score 604.5; DB 1; Length 123;
Best Local Similarity 99.2%; Pred. No. 2e-56;
Matches 122; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY      1 MKLKVTVNGTAYDVDVDVKSHENPMGTILFGGGTGGAPAP-AAGGAGAGKAGEGEIPAP 59
Db      1 MKLKVTVNGTAYDVDVDVKSHENPMGTILFGGGTGGAPAPRAAGGAGAGKAGEGEIPAP 60

QY      60 LAGTVSKILVKEGDTVKGQTVLVLEAMKMETEINAPTDGKVEKVLVKERDAVQGGQGLI 119
Db      61 LAGTVSKILVKEGDTVKGQTVLVLEAMKMETEINAPTDGKVEKVLVKERDAVQGGQGLI 120

QY      120 KIG 122
Db      121 KIG 123

RESULT 4
US-08-476-537-107
; Sequence 107, Application US/08476537
; Patent No. 5756290
; GENERAL INFORMATION:
; APPLICANT: Robert Haselkorn and Piotr Gornicki
; TITLE OF INVENTION: Cyanobacterial and Plant Acetyl-CoA
; TITLE OF INVENTION: Carboxylase
; NUMBER OF SEQUENCES: 116
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: 321 No. 5756290th Clark Street
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60610
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII-DOS
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/476,537
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/956,700
; FILING DATE: 10/21/92
; ATTORNEY/AGENT INFORMATION:
; NAME: Thomas E. No. 5756290thrup
; REGISTRATION NUMBER: 33,268
; REFERENCE/DOCKET NUMBER: ARCD:058
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 1-312-744-0090
; TELEFAX: 1-312-755-4489
; INFORMATION FOR SEQ ID NO: 107:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 123 amino acids
; TYPE: Amino acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; MOLECULE TYPE: Peptide
US-08-476-537-107
Query Match      98.3%; Score 604.5; DB 1; Length 123;
Best Local Similarity 99.2%; Pred. No. 2e-56;
Matches 122; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY      1 MKLKVTVNGTAYDVDVDVKSHENPMGTILFGGGTGGAPAP-AAGGAGAGKAGEGEIPAP 59
Db      1 MKLKVTVNGTAYDVDVDVKSHENPMGTILFGGGTGGAPAPRAAGGAGAGKAGEGEIPAP 60
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QY 60 LAGTVSKILVKEGDTVKGQTVLVLEAMKMETEINAPTDGKVEKVLVKERDAVQGGQGLI 119
Db 61 LAGTVSKILVKEGDTVKGQTVLVLEAMKMETEINAPTDGKVEKVLVKERDAVQGGQGLI 120
QY 120 KIG 122
Db 121 KIG 123

RESULT 5
US-08-485-607-107
; Sequence 107, Application US/08485607
; Patent No. 5972627
; GENERAL INFORMATION:
; APPLICANT: Robert Haselkorn and Piotr Gornicki
; TITLE OF INVENTION: Cyanobacterial and Plant Acetyl-CoA
; TITLE OF INVENTION: Carboxylase
; NUMBER OF SEQUENCES: 116
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: 321 No. 5792627th Clark Street
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60610

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII-DOS
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,607
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/956,700
; FILING DATE: 10/21/92

; ATTORNEY/AGENT INFORMATION:
; NAME: Thomas E. No. 5792627thrup
; REGISTRATION NUMBER: 33,268
; REFERENCE/DOCKET NUMBER: ARCD:058
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 1-312-744-0090
; TELEFAX: 1-312-755-4489
; INFORMATION FOR SEQ ID NO: 107:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 123 amino acids
; TYPE: Amino acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; MOLECULE TYPE: Peptide
US-08-485-607-107

Query Match 98.3%; Score 604.5; DB 1; Length 123;
Best Local Similarity 99.2%; Pred. No. 2e-56;
Matches 122; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 1 MKLKVTVNGTAYDVDVDKSHENPMGTILFGGGTGGAPAP-AAGGAGAGKAGEGEIPAP 59
Db 1 MKLKVTVNGTAYDVDVDKSHENPMGTILFGGGTGGAPAPRAAGGAGAGKAGEGEIPAP 60

QY 60 LAGTVSKILVKEGDTVKGQTVLVLEAMKMETEINAPTDGKVEKVLVKERDAVQGGQGLI 119
Db 61 LAGTVSKILVKEGDTVKGQTVLVLEAMKMETEINAPTDGKVEKVLVKERDAVQGGQGLI 120
QY 120 KIG 122
Db 121 KIG 123

RESULT 6
US-08-475-879-107
; Sequence 107, Application US/08475879

; Patent No. 5972644
; Patent No. 5972644 5786170
; GENERAL INFORMATION:
; APPLICANT: Robert Haselkorn and Piotr Gornicki
; TITLE OF INVENTION: Cyanobacterial and Plant Acetyl-CoA
; TITLE OF INVENTION: Carboxylase
; NUMBER OF SEQUENCES: 116
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: 321 No. 5972644 5786170th Clark Street
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60610

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII-DOS
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/475,879
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/956,700
; FILING DATE: 10/21/92

; ATTORNEY/AGENT INFORMATION:
; NAME: Thomas E. No. 5972644 5786170thrup
; REGISTRATION NUMBER: 33,268
; REFERENCE/DOCKET NUMBER: ARCD:058
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 1-312-744-0090
; TELEFAX: 1-312-755-4489
; INFORMATION FOR SEQ ID NO: 107:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 123 amino acids
; TYPE: Amino acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; MOLECULE TYPE: Peptide
US-08-475-879-107

Query Match 98.3%; Score 604.5; DB 2; Length 123;
Best Local Similarity 99.2%; Pred. No. 2e-56;
Matches 122; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 1 MKLKVTVNGTAYDVDVDKSHENPMGTILFGGGTGGAPAP-AAGGAGAGKAGEGEIPAP 59
Db 1 MKLKVTVNGTAYDVDVDKSHENPMGTILFGGGTGGAPAPRAAGGAGAGKAGEGEIPAP 60
QY 60 LAGTVSKILVKEGDTVKGQTVLVLEAMKMETEINAPTDGKVEKVLVKERDAVQGGQGLI 119
Db 61 LAGTVSKILVKEGDTVKGQTVLVLEAMKMETEINAPTDGKVEKVLVKERDAVQGGQGLI 120
QY 120 KIG 122
Db 121 KIG 123

RESULT 7
US-07-687-819-1
; Sequence 1, Application US/07687819
; Patent No. 5972639
; GENERAL INFORMATION:
; APPLICANT: Haase, Ferdinand C.
; APPLICANT: Cress, Dean E.
; TITLE OF INVENTION: Carrier Protein
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rohm and Haas Company
; STREET: Independence Mall West
; CITY: Philadelphia
; STATE: PA

COUNTRY: USA
ZIP: 19105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/687,819
FILING DATE: 19910520
CLASSIFICATION: 530
CLASSIFICATION: C07K13/00
CLASSIFICATION: C07K15/26
CLASSIFICATION: C12P21/00
CLASSIFICATION: 424/85.7
CLASSIFICATION: 530/351
CLASSIFICATION: 435/69.51
ATTORNEY/AGENT INFORMATION:
NAME: Driks, Jordan J.
REGISTRATION NUMBER: 22,029
REFERENCE/DOCKET NUMBER: 89-020
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-592-2478
TELEFAX: 215-592-2682
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 123 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Propionibacterium shermanii
PUBLICATION INFORMATION:
AUTHORS: Maloy, W L
AUTHORS: Bowien, B U
AUTHORS: Zwolinski, G K
AUTHORS: Kumar, K G
AUTHORS: Wood, H G
TITLE: Amino Acid Sequence of the Biotinyl Subunit
Patent No. 6072039
TITLE: from Transcarboxylase
JOURNAL: Journal of Biological Chemistry
VOLUME: 254
ISSUE: 22
PAGES: 11615-11622
DATE: No. 6072039 26-1979
RELEVANT RESIDUES IN SEQ ID NO: 1: FROM 1 TO 123
US-07-687-819-1

Query Match 98.3%; Score 604.5; DB 3; Length 123;
Best Local Similarity 99.2%; Pred. No. 2e-56;
Matches 122; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 1 MKLKVTVNGTAYDVDVDKSHENPMGTILFGGGTGGAPAP-AAGGAGAGKAGEGEIPAP 59
Db 1 MKLKVTVNGTAYDVDVDKSHENPMGTILFGGGTGGAPAPRAAGGAGAGKAGEGEIPAP 60
QY 60 LAGTVSKILVKEGDTVKGQTVLVLEAMKMETEINAPTDGKVEKVLVKERDAVQGGQGLI 119
Db 61 LAGTVSKILVKEGDTVKGQTVLVLEAMKMETEINAPTDGKVEKVLVKERDAVQGGQGLI 120

QY 120 KIG 122
Db 121 KIG 123

RESULT 8
US-09-433-043B-107
Sequence 107, Application US/09433043B
Patent No. 6399342
GENERAL INFORMATION:
APPLICANT: HASELKORN, ROBERT
APPLICANT: GORNICKI, PIOTR

TITLE OF INVENTION: CYANOBACTERIAL AND PLANT ACETYL-CoA CARBOXYLASE
FILE REFERENCE: ARCD:338US
CURRENT APPLICATION NUMBER: US/09/433,043B
CURRENT FILING DATE: 1999-10-25
PRIOR APPLICATION NUMBER: 08/475,879
PRIOR FILING DATE: 1995-06-07
PRIOR APPLICATION NUMBER: 07/956,700
PRIOR FILING DATE: 1992-10-02
NUMBER OF SEQ ID NOS: 128
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 107
LENGTH: 123
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: Peptide
US-09-433-043B-107

Query Match 98.3%; Score 604.5; DB 4; Length 123;
Best Local Similarity 99.2%; Pred. No. 2e-56;
Matches 122; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 MKLKVTVNGTAYDVDVDKSHENPMGTILFGGGTGGAPAP-AAGGAGAGKAGEGEIPAP 59
Db 1 MKLKVTVNGTAYDVDVDKSHENPMGTILFGGGTGGAPAPRAAGGAGAGKAGEGEIPAP 60
QY 60 LAGTVSKILVKEGDTVKGQTVLVLEAMKMETEINAPTDGKVEKVLVKERDAVQGGQGLI 119
Db 61 LAGTVSKILVKEGDTVKGQTVLVLEAMKMETEINAPTDGKVEKVLVKERDAVQGGQGLI 120
QY 120 KIG 122
Db 121 KIG 123

RESULT 9
US-09-433-043B-128
Sequence 128, Application US/09433043B
Patent No. 6399342
GENERAL INFORMATION:
APPLICANT: HASELKORN, ROBERT
APPLICANT: GORNICKI, PIOTR
TITLE OF INVENTION: CYANOBACTERIAL AND PLANT ACETYL-CoA CARBOXYLASE
FILE REFERENCE: ARCD:338US
CURRENT APPLICATION NUMBER: US/09/433,043B
CURRENT FILING DATE: 1999-10-25
PRIOR APPLICATION NUMBER: 08/475,879
PRIOR FILING DATE: 1995-06-07
PRIOR APPLICATION NUMBER: 07/956,700
PRIOR FILING DATE: 1992-10-02
NUMBER OF SEQ ID NOS: 128
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 128
LENGTH: 123
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: Peptide
US-09-433-043B-128

Query Match 97.3%; Score 598.5; DB 4; Length 123;
Best Local Similarity 98.4%; Pred. No. 8.6e-56;
Matches 121; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 MKLKVTVNGTAYDVDVDKSHENPMGTILFGGGTGGAPAP-AAGGAGAGKAGEGEIPAP 59
Db 1 MKLKVTVNGTAYDVDVDKSHENPMGTILFGGGTGGAPAPRAAGGAGAGKAGEGEIPAP 60
QY 60 LAGTVSKILVKEGDTVKGQTVLVLEAMKMETEINAPTDGKVEKVLVKERDAVQGGQGLI 119
Db 61 LAGTVSKILVKEGDTVKGQTVLVLEAMKMETEINAPTDGKVEKVLVKERDAVQGGQGLI 120

QY 120 KIG 122
Db 121 HIG 123

RESULT 10
5252466-6
; APPLICANT: CRONAN, JOHN E.
; TITLE OF INVENTION: FUSION PROTEINS HAVING A SITE FOR IN
; VIVO POST-TRANSLATION MODIFICATION AND METHODS OF MAKING AND
; PURIFYING THEM
; NUMBER OF SEQUENCES: 24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/525,568
; FILING DATE: 18-MAY-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 354,266
; FILING DATE: 19-MAY-1989
; SEQ ID NO:6:
; LENGTH: 106
5252466-6

Query Match 84.3%; Score 518.5; DB 6; Length 106;
Best Local Similarity 99.1%; Pred. No. 1.9e-47;
Matches 105; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 18 VDKSHENPMGTILFGGGTGGAPAP-AAGGAGAGKAGEGEIPAPLAGTVSKILVKEGDTVK 76
Db 1 VDKSHENPMGTILFGGGTGGAPAPRAAGGAGAGKAGEGEIPAPLAGTVSKILVKEGDTVK 60

QY 77 AGQTVLVLEAMKMETEINAPTDGKVEKVLVKERDAVQGGGLIKIG 122
Db 61 AGQTVLVLEAMKMETEINAPTDGKVEKVLVKERDAVQGGGLIKIG 106

RESULT 11
5252466-1
; APPLICANT: CRONAN, JOHN E.
; TITLE OF INVENTION: FUSION PROTEINS HAVING A SITE FOR IN
; VIVO POST-TRANSLATION MODIFICATION AND METHODS OF MAKING AND
; PURIFYING THEM
; NUMBER OF SEQUENCES: 24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/525,568
; FILING DATE: 18-MAY-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 354,266
; FILING DATE: 19-MAY-1989
; SEQ ID NO:1:
; LENGTH: 66
5252466-1

Query Match 50.4%; Score 310; DB 6; Length 66;
Best Local Similarity 97.0%; Pred. No. 9.8e-26;
Matches 64; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 57 PAPLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVLVKERDAVQGGQ 116
Db 1 PAPLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVLVKERDAVQGGQ 60

QY 117 GLIKIG 122
Db 61 GLIKIG 66

RESULT 12
US-07-687-819-2
; Sequence 2, Application US/07687819
; Patent No. 6072039
; GENERAL INFORMATION:

; APPLICANT: Haase, Ferdinand C.
; APPLICANT: Cress, Dean E.
; TITLE OF INVENTION: Carrier Protein
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rohm and Haas Company
; STREET: Independence Mall West
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/687,819
; FILING DATE: 19910520
; CLASSIFICATION: 530
; CLASSIFICATION: C07K13/00
; CLASSIFICATION: C07K15/26
; CLASSIFICATION: C12P21/00
; CLASSIFICATION: 424/85.7
; CLASSIFICATION: 530/351
; CLASSIFICATION: 435/69.51
; ATTORNEY/AGENT INFORMATION:
; NAME: Driks, Jordan J.
; REGISTRATION NUMBER: 22,029
; REFERENCE/DOCKET NUMBER: 89-020
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-592-2478
; TELEFAX: 215-592-2682
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 43 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-07-687-819-2

Query Match 34.3%; Score 211; DB 3; Length 43;
Best Local Similarity 100.0%; Pred. No. 1.5e-15;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 57 PAPLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDG 99
Db 1 PAPLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDG 43

RESULT 13
US-09-433-043B-127
; Sequence 127, Application US/09433043B
; Patent No. 6399342
; GENERAL INFORMATION:
; APPLICANT: HASELKORN, ROBERT
; APPLICANT: GORNICKI, PIOTR
; TITLE OF INVENTION: CYANOACTERIAL AND PLANT ACETYL-CoA CARBOXYLASE
; FILE REFERENCE: ARCD:338US
; CURRENT APPLICATION NUMBER: US/09/433,043B
; CURRENT FILING DATE: 1999-10-25
; PRIOR APPLICATION NUMBER: 08/475,879
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: 07/956,700
; PRIOR FILING DATE: 1992-10-02
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 127
; LENGTH: 170
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:


```

;
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII-DOS
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,607
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/956,700
; FILING DATE: 10/21/92
; ATTORNEY/AGENT INFORMATION:
; NAME: Thomas E. No. 5792627thrup
; REGISTRATION NUMBER: 33,268
; REFERENCE/DOCKET NUMBER: ARCD:058
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 1-312-744-0090
; TELEFAX: 1-312-755-4489
; INFORMATION FOR SEQ ID NO: 106:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 165 amino acids
; TYPE: Amino acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; MOLECULE TYPE: Peptide
;
US-08-485-607-106

Query Match 32.6%; Score 200.5; DB 1; Length 165;
Best Local Similarity 52.9%; Pred. No. 1.1e-13;
Matches 45; Conservative 10; Mismatches 29; Indels 1; Gaps 1;

QY 38 APAPAGGAGAGKAGEG-EIPAPLAGTVSKILVKEGDTVKGQTVLVLEAMKMETEINAP 96
Db 80 APAPASAPAAAPAGAGTPTVAPLAGTIWKVLASEGQTVAAAGEVLLILEAMKMETEIRAA 139

QY 97 TDGKVEKVLVKERDAVQGGGLIKI 121
Db 140 QAGTVRGIAVKAGDAVAVGDTLMTL 164

RESULT 17
US-08-475-879-106
; Sequence 106, Application US/08475879
; Patent No. 5972644
; Patent No. 5972644 5786170
; GENERAL INFORMATION:
; APPLICANT: Robert Haselkorn and Piotr Gornicki
; TITLE OF INVENTION: Cyanobacterial and Plant Acetyl-CoA
; TITLE OF INVENTION: Carboxylase
; NUMBER OF SEQUENCES: 116
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: 321 No. 5972644 5786170th Clark Street
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60610
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII-DOS
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/475,879
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/956,700
; FILING DATE: 10/21/92
; ATTORNEY/AGENT INFORMATION:
; NAME: Thomas E. No. 5972644 5786170thrup
; REGISTRATION NUMBER: 33,268
; REFERENCE/DOCKET NUMBER: ARCD:058
; TELECOMMUNICATION INFORMATION:
;

```

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;
; TELEPHONE: 1-312-744-0090
; TELEFAX: 1-312-755-4489
; INFORMATION FOR SEQ ID NO: 106:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 165 amino acids
; TYPE: Amino acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; MOLECULE TYPE: Peptide
;
US-08-475-879-106

Query Match 32.6%; Score 200.5; DB 2; Length 165;
Best Local Similarity 52.9%; Pred. No. 1.1e-13;
Matches 45; Conservative 10; Mismatches 29; Indels 1; Gaps 1;

QY 38 APAPAGGAGAGKAGEG-EIPAPLAGTVSKILVKEGDTVKGQTVLVLEAMKMETEINAP 96
Db 80 APAPASAPAAAPAGAGTPTVAPLAGTIWKVLASEGQTVAAAGEVLLILEAMKMETEIRAA 139

QY 97 TDGKVEKVLVKERDAVQGGGLIKI 121
Db 140 QAGTVRGIAVKAGDAVAVGDTLMTL 164

RESULT 18
US-09-433-043B-106
; Sequence 106, Application US/09433043B
; Patent No. 6399342
; GENERAL INFORMATION:
; APPLICANT: HASELKORN, ROBERT
; APPLICANT: GORNICKI, PIOTR
; TITLE OF INVENTION: CYANOBACTERIAL AND PLANT ACETYL-CoA CARBOXYLASE
; FILE REFERENCE: ARCD:338US
; CURRENT APPLICATION NUMBER: US/09/433,043B
; CURRENT FILING DATE: 1999-10-25
; PRIOR APPLICATION NUMBER: 08/475,879
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: 07/956,700
; PRIOR FILING DATE: 1992-10-02
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 106
; LENGTH: 165
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
;
US-09-433-043B-106

Query Match 32.6%; Score 200.5; DB 4; Length 165;
Best Local Similarity 52.9%; Pred. No. 1.1e-13;
Matches 45; Conservative 10; Mismatches 29; Indels 1; Gaps 1;

QY 38 APAPAGGAGAGKAGEG-EIPAPLAGTVSKILVKEGDTVKGQTVLVLEAMKMETEINAP 96
Db 80 APAPASAPAAAPAGAGTPTVAPLAGTIWKVLASEGQTVAAAGEVLLILEAMKMETEIRAA 139

QY 97 TDGKVEKVLVKERDAVQGGGLIKI 121
Db 140 QAGTVRGIAVKAGDAVAVGDTLMTL 164

RESULT 19
5252466-19
; Patent No. 5252466
; APPLICANT: CRONAN, JOHN E.
; TITLE OF INVENTION: FUSION PROTEINS HAVING A SITE FOR IN
; VIVO POST-TRANSLATION MODIFICATION AND METHODS OF MAKING AND
; PURIFYING THEM
; NUMBER OF SEQUENCES: 24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/525,568
;

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; FILING DATE: 18-MAY-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 354,266
; FILING DATE: 19-MAY-1989
; SEQ ID NO:19:
; LENGTH: 100
5252466-19

Query Match      31.5%; Score 193.5; DB 6; Length 100;
Best Local Similarity 51.8%; Pred. No. 3.1e-13;
Matches 44; Conservative 10; Mismatches 30; Indels 1; Gaps 1;

QY 38 APAPAGGAGAGKAGG-EIPAPLAGTGVSKILVKEGDTVKAGQTVLVLEAMKMETEINAP 96
Db 15 APAPASAPAAAAPAGAGTPTVAPLAGFTWKVLASEGQTVAAAGEVLLILEAMKMETEIRAA 74

QY 97 TDGKVEKVLVKERDAVQGGGLIKI 121
Db 75 QAGTVRGIAVKAGDAVAVGDTLMTL 99

RESULT 20
US-09-134-000C-6221
; Sequence 6221, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6221
; LENGTH: 147
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-134-000C-6221

Query Match      28.5%; Score 175.5; DB 4; Length 147;
Best Local Similarity 37.2%; Pred. No. 4e-11;
Matches 48; Conservative 17; Mismatches 55; Indels 9; Gaps 2;

QY 2 KLVTVNGTAYDVVD-----VDKSHENPMGTILFGGGTGGA-PAAGGAGAGKAG 52
Db 18 KFKISIDGKEYLVEMERIGVPPAPAPVAPQPTAPVATTETPAPAVEETPASAAPAG 77

QY 53 EGEIPAPLAGTGVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVLVKERDAV 112
Db 78 ADAMPAPMPGTVLKVLNVGDTVSENQPLLLILEAMKMEINEIVAGKAGTGTGIHVTQGIIV 137

QY 113 QGGQGLIKI 121
Db 138 NPGEPLITI 146

RESULT 21
US-09-252-991A-19134
; Sequence 19134, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
```

```
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 19134
; LENGTH: 612
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-19134

Query Match      27.4%; Score 168.5; DB 4; Length 612;
Best Local Similarity 32.4%; Pred. No. 1.3e-09;
Matches 44; Conservative 20; Mismatches 43; Indels 29; Gaps 3;

QY 5 VTVNGTAYDVVD-----DVKDSHE-----NPMGTILFGGGTGGA-PAAGG 45
Db 485 IDVHGETYRVDITGVGVKSDNKRHFYLSIDGMPEEVVFEPLNEYVAGSASGRKHA----- 539

QY 46 AGAKAGAGEGEIPAPLAGTGVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVL 105
Db 540 -----SEPGHVSTTTPGNIVDLVKEGDSVKAGQAVLITEAMKMETEQVQAGIAGTVKAIH 594

QY 106 VKERDAVQGGGLIKI 121
Db 595 VAKGDRVNPGEILIEI 610

RESULT 22
US-09-220-081-2
; Sequence 2, Application US/092200081
; Patent No. 6171833
; GENERAL INFORMATION:
; APPLICANT: Sinskey, Anthony J.
; APPLICANT: Lessard, Philip A.
; APPLICANT: Willis, Laura B.
; APPLICANT: Stephanopoulos, Gregory
; TITLE OF INVENTION: Pyruvate Carboxylase from Corynebacterium glutamicum
; FILE REFERENCE: 1533.0790000
; CURRENT APPLICATION NUMBER: US/09/220,081
; CURRENT FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1140
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-220-081-2

Query Match      25.9%; Score 159.5; DB 3; Length 1140;
Best Local Similarity 43.2%; Pred. No. 2.5e-08;
Matches 32; Conservative 15; Mismatches 26; Indels 1; Gaps 1;

QY 48 AGKAGEGEIPAPLAGTGVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVLVK 107
Db 1067 ADSSNKGHVAAFPAGVVT-VTVAEDEGVKAGDAVAIIIEAMKMEATITASVDGKIDRVVVP 1125

QY 108 ERDAVQGGGLIKI 121
Db 1126 AATKVEGGDLIVVV 1139

RESULT 23
US-09-677-575-2
; Sequence 2, Application US/09677575
; Patent No. 6403351
; GENERAL INFORMATION:
; APPLICANT: Sinskey, Anthony J.
; APPLICANT: Lessard, Philip A.
; APPLICANT: Willis, Laura B.
; APPLICANT: Stephanopoulos, Gregory
; TITLE OF INVENTION: Pyruvate Carboxylase from Corynebacterium glutamicum
; FILE REFERENCE: 1533.0790000
; CURRENT APPLICATION NUMBER: US/09/677,575
; CURRENT FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 09/220,081
```

; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1140
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-677-575-2

Query Match 25.9%; Score 159.5; DB 4; Length 1140;
Best Local Similarity 43.2%; Pred. No. 2.5e-08;
Matches 32; Conservative 15; Mismatches 26; Indels 1; Gaps 1;

QY 48 AGKAGEGEIPAPLAGTIVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVLVK 107
Db 1067 ADSSNKGHVAAFPAGVVT-VTVAEGDEVKAGDAVAIIEMKMEATITASVDGKIDRVVVP 1125

QY 108 ERDAVQGGGLIKI 121
Db 1126 AATKVEGGDLIVVV 1139

RESULT 24
US-09-328-352-5587
; Sequence 5587, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 5587
; LENGTH: 652
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-5587

Query Match 24.9%; Score 153; DB 4; Length 652;
Best Local Similarity 45.9%; Pred. No. 6.1e-08;
Matches 34; Conservative 15; Mismatches 25; Indels 0; Gaps 0;

QY 48 AGKAGEGEIPAPLAGTIVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVLVK 107
Db 577 ADVAGDGKIRAPMDGAVVNILVKNKGQVTKGQTLVLEAMKIQQIKSDVDGVVDEILGQ 636

QY 108 ERDAVQGGGLIKI 121
Db 637 GQQVKRQMLFSI 650

RESULT 25
US-09-252-991A-27999
; Sequence 27999, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 27999
; LENGTH: 701
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-27999

Query Match 24.7%; Score 152; DB 4; Length 701;
Best Local Similarity 42.1%; Pred. No. 8.5e-08;
Matches 32; Conservative 18; Mismatches 26; Indels 0; Gaps 0;

QY 46 AGAKAGEGEIPAPLAGTIVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVL 105
Db 621 AEAHAHQGGLSAPMNGSIVRVLPVPGQTVVAGATLVVLEAMKMEHSIRAPHAGVVVKALY 680

QY 106 VKERDAVQGGGLIKI 121
Db 681 CSEGELVEEGTPLVEL 696

RESULT 26
US-08-997-080-166
; Sequence 166, Application US/08997080
; Patent No. 5968524
; GENERAL INFORMATION:
; APPLICANT: WATSON, JAMES D.
; APPLICANT: TAN, PAUL L.J.
; TITLE OF INVENTION: METHODS AND COMPOUNDS FOR THE TREATMENT OF IMMUNOLOGICALLY-
; NUMBER OF SEQUENCES: 194
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Ann W. Speckman
; STREET: 2601 Elliott Avenue, Suite 4185
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/997,080
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Sleath, Janet
; REGISTRATION NUMBER: 37,007
; REFERENCE/DOCKET NUMBER: 11000.1007
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-269-0565
; TELEFAX: 206-269-0563
; TELEX:
; INFORMATION FOR SEQ ID NO: 166:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 108 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-997-080-166

Query Match 24.4%; Score 150; DB 2; Length 108;
Best Local Similarity 46.5%; Pred. No. 1.3e-08;
Matches 33; Conservative 10; Mismatches 28; Indels 0; Gaps 0;

QY 52 GEGEIPAPLAGTIVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVLKERDA 111
Db 33 GDERVDAPFASVWKVDVAVGDRVVAGQPLIALVLEAMKMETVLRAPADGVVTQILVSAGHL 92

QY 112 VQGGGLIKIG 122
Db 93 VDPGTPLVVVG 103

RESULT 27

;;
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/095,855
;; FILING DATE:
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/705,347
;; FILING DATE: 29-AUG-1996
;; APPLICATION NUMBER: 08/873,970
;; FILING DATE: 12-JUN-1997
;; APPLICATION NUMBER: 08/997,362
;; FILING DATE: 23-DEC-1997
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Sleath, Janet
;; REGISTRATION NUMBER: 37,007
;; REFERENCE/DOCKET NUMBER: 11000.1002c3
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 206-269-0565
;; TELEFAX: 206-269-0563
;; TELEX:
;; INFORMATION FOR SEQ ID NO: 199:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 243 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-09-095-855-199

Query Match 24.4%; Score 150; DB 3; Length 243;
Best Local Similarity 46.5%; Pred. No. 3.6e-08;
Matches 33; Conservative 10; Mismatches 28; Indels 0; Gaps 0;

QY 52 GGEIPAPLAGTVSKILVKEGDTVKGQTVLVLEAMKMETEINAPTDGKVKVLVKERDA 111
Db 168 GDERVDAPFASVWKVDVAVGDRVVAGQPLLALAMKMETVLRAPADGVVTTQILVSAGHL 227

QY 112 VQGGQGLIKIG 122
Db 228 VDPGTPLVVVG 238

RESULT 33
US-09-205-426-199
; Sequence 199, Application US/09205426
; Patent No. 6406704
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Tan, Paul L. J.
; TITLE OF INVENTION: Compounds and Methods for Treatment and
; TITLE OF INVENTION: Diagnosis of Mycobacterial Infections
; FILE REFERENCE: 11000.1002c4
; CURRENT APPLICATION NUMBER: US/09/205,426
; CURRENT FILING DATE: 1998-12-04
; EARLIER APPLICATION NUMBER: 09/095,855
; EARLIER FILING DATE: 1998-06-11
; EARLIER APPLICATION NUMBER: 08/997,362
; EARLIER FILING DATE: 1997-12-23
; EARLIER APPLICATION NUMBER: 08/873,970
; EARLIER FILING DATE: 1997-06-12
; EARLIER APPLICATION NUMBER: 08/705,347
; EARLIER FILING DATE: 1996-08-29
; NUMBER OF SEQ ID NOS: 208
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 199
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Mycobacterium vaccae
; US-09-205-426-199

Query Match 24.4%; Score 150; DB 4; Length 243;
Best Local Similarity 46.5%; Pred. No. 3.6e-08;
Matches 33; Conservative 10; Mismatches 28; Indels 0; Gaps 0;

QY 52 GGEIPAPLAGTVSKILVKEGDTVKGQTVLVLEAMKMETEINAPTDGKVKVLVKERDA 111
Db 168 GDERVDAPFASVWKVDVAVGDRVVAGQPLLALAMKMETVLRAPADGVVTTQILVSAGHL 227
QY 112 VQGGQGLIKIG 122
Db 228 VDPGTPLVVVG 238
RESULT 34
US-09-134-001C-3428
; Sequence 3428, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 3428
; LENGTH: 1154
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
; US-09-134-001C-3428

Query Match 24.2%; Score 149; DB 4; Length 1154;
Best Local Similarity 27.8%; Pred. No. 3.3e-07;
Matches 40; Conservative 23; Mismatches 41; Indels 40; Gaps 3;

QY 8 NGTAYDVVD-----VDKSHENPMGTILFGGGTGGAPAPAGGAG-----47
Db 1017 NGETVEIEIDTGKRLIIKLETISEPDENGKRTIYY-----AMNGQARRIYIQDEN 1066

QY 48 -----AKGAGEGEIPAPLAGTVSKILVKEGDTVKGQTVLVLEAMKMETEINAPT 97
Db 1067 VKTNANVKPKADKSNPNHIGAQMPSVTEVKSVGVDEVQANQPLLITEAMKMETTIQAPF 1126

QY 98 DGKVEKVLVKERDAVQGGQGLIKI 121
Db 1127 DGIKQINVANGDAIATGDLLEI 1150

RESULT 35
US-09-252-991A-26143
; Sequence 26143, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 26143
; LENGTH: 676
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
; US-09-252-991A-26143

Query Match 24.1%; Score 148.5; DB 4; Length 676;
Best Local Similarity 35.7%; Pred. No. 1.9e-07;
Matches 41; Conservative 16; Mismatches 43; Indels 15; Gaps 2;

QY 11 AYDVEDVDKSHENPMGTILFGGTGG----APAPAGGAGAGKAGEGEIPAPLAGTVSK 66
Db 569 AYHVD-----GGRLWVYGHGNNLELVEVTHAGASAQVGASSGTLKAPMDGAIVE 617
QY 67 ILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVLVKERDAVQGGQGLIKI 121
Db 618 VLVGEGERVKGQLLVLEAMKMEHPLKAGVDGVVRRVQVGRGEQVRNRQVLVEV 672

RESULT 36
US-09-673-395A-230
; Sequence 230, Application US/09673395A
; Patent No. 6620923
; GENERAL INFORMATION:
; APPLICANT: SPECHT, THOMAS
; APPLICANT: HINZMANN, BERND
; APPLICANT: SCHMITT, ARMIN
; APPLICANT: PILARSKY, CHRISTIAN
; APPLICANT: DAHL, EDGAR
; APPLICANT: ROSENTHAL, ANDRE
; TITLE OF INVENTION: HUMAN NUCLEIC ACID SEQUENCES FROM UTERUS TUMOR TISSUE
; FILE REFERENCE: ALBRE-12
; CURRENT APPLICATION NUMBER: US/09/673,395A
; CURRENT FILING DATE: 2000-10-17
; NUMBER OF SEQ ID NOS: 637
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 230
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-673-395A-230

Query Match 23.9%; Score 147; DB 4; Length 117;
Best Local Similarity 42.9%; Pred. No. 3e-08;
Matches 30; Conservative 14; Mismatches 26; Indels 0; Gaps 0;

QY 39 PAPAAGGAGAGKAGEGEIPAPLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTD 98
Db 24 PVPKYLSSVSSQETQGGPLAPMTGTIEKFVFKAGDKVKAGDSLVMVMIAMKMEHTIKSPKD 83
QY 99 GKVEKVLVKE 108
Db 84 GTVKVVFYRE 93

RESULT 37
US-09-134-000C-5707
; Sequence 5707, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5707
; LENGTH: 1163
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-134-000C-5707

Query Match 23.4%; Score 144; DB 4; Length 1163;
Best Local Similarity 43.3%; Pred. No. 1.1e-06;
Matches 29; Conservative 17; Mismatches 21; Indels 0; Gaps 0;
QY 55 EIPAPLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVLVKERDAVQG 114

Db 1094 QIGATMSGSVLQVLVKRGDKVEKGQPLLITEAMKMETTIEARFAGTVDHIYVEGEAISS 1153
QY 115 GQGLIKI 121
Db 1154 GDLLLEV 1160

RESULT 38
US-09-134-000C-4552
; Sequence 4552, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4552
; LENGTH: 168
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-134-000C-4552

Query Match 22.7%; Score 139.5; DB 4; Length 168;
Best Local Similarity 40.5%; Pred. No. 2.9e-07;
Matches 30; Conservative 12; Mismatches 25; Indels 7; Gaps 1;

QY 55 EIPAPLAGTV-----SKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVLVK 107
Db 91 EITSPIVGIVLQAPADKENFVKGDTVKTGDDVVCIVEAMKLMNEITATVDGVITEILVN 150
QY 108 ERDAVQGGQGLIKI 121
Db 151 NEDVVEFGQPLFRV 164

RESULT 39
5252466-5
; Patent No. 5252466
; APPLICANT: CRONAN, JOHN E.
; TITLE OF INVENTION: FUSION PROTEINS HAVING A SITE FOR IN
; VIVO POST-TRANSLATION MODIFICATION AND METHODS OF MAKING AND
; PURIFYING THEM
; NUMBER OF SEQUENCES: 24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/525,568
; FILING DATE: 18-MAY-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 354,266
; FILING DATE: 19-MAY-1989
; SEQ ID NO: 5
; LENGTH: 67
5252466-5

Query Match 22.3%; Score 137; DB 6; Length 67;
Best Local Similarity 50.0%; Pred. No. 1.7e-07;
Matches 29; Conservative 10; Mismatches 19; Indels 0; Gaps 0;

QY 58 APLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVLVKERDAVQGG 115
Db 2 APMVGLEVKVLKDGKQVQEGQFVLVLEAMKMEHVVKAPANGYVSGLEIKVQGSVDG 59

RESULT 40
US-08-611-107-4
; Sequence 4, Application US/08611107
; Patent No. 5801233
; GENERAL INFORMATION:

APPLICANT: Haselkorn, Robert
APPLICANT: Gornicki, Piotr
TITLE OF INVENTION: NUCLEIC ACID COMPOSITIONS ENCODING
TITLE OF INVENTION: ACETYL-CoA CARBOXYLASE AND USES
TITLE OF INVENTION: THEREFOR
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: United States of America
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/611,107
FILING DATE: Concurrently Herewith
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US SN 07/956,700
FILING DATE: 02-OCT-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US PCT/US93/09340
FILING DATE: 30-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US SN 08/422,560
FILING DATE: 14-APR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: ARCD:221
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 158 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-611-107-4

Query Match 22.2%; Score 136.5; DB 1; Length 158;
Best Local Similarity 35.5%; Pred. No. 5.6e-07;
Matches 33; Conservative 16; Mismatches 35; Indels 9; Gaps 2;

QY 38 APAPAGGAGAGKAGEG--EIPAPLAGTVSKI-----LVKEGDTVKAGQTVLVLEAMK 88
Db 63 APTPAAAPPAGPLGGKFLKITAPMVGTFFYRAPAPAPPEPPFVNVGDRIQVGQTVLCILEAMK 122
QY 89 METEINAPTDGKVEKVLVKERDAVQGGGLIKI 121
Db 123 LMNELESEVTGEVVEILVQNGEPVEFNQPLFRL 155

Search completed: March 3, 2004, 10:32:34
Job time : 22.3333 secs

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OM protein - protein search, using sw model

Run on: March 3, 2004, 10:23:49 ; Search time 36.4583 Seconds
(without alignments)
542.491 Million cell updates/sec

Title: US-09-987-485a-2
Perfect score: 342
Sequence: 1 EGEIPAPLAGTGVSKILVKEG.....KVLVKERDAVQGGQLIKIG 70

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	342	100.0	70	ABG72299	Abg72299 Escherich
2	342	100.0	122	ABG72298	Abg72298 Escherich
3	342	100.0	123	AAR28177	Aar28177 1.3S poly
4	342	100.0	126	AAAY84002	Aay84002 Amino aci
5	342	100.0	194	AAAY78908	Aay78908 Outer sur
6	342	100.0	253	AAAW11886	Aaw11886 Hantaviru
7	342	100.0	256	AAAY84001	Aay84001 Amino aci
8	342	100.0	266	AAAY84003	Aay84003 Amino aci
9	263	76.9	125	AAU51122	Aau51122 Propionib
10	263	76.9	125	ABM47641	Abm47641 Putative
11	195	57.0	148	AAAB96610	Aab96610 Putative
12	174	50.9	1148	ABU18942	Abu18942 Protein e
13	172	50.3	143	ABU21035	Abu21035 Protein e
14	167	48.8	1144	ABU24164	Abu24164 Protein e
15	166	48.5	596	ABU33366	Abu33366 Protein e
16	165	48.2	588	ABU32216	Abu32216 Protein e
17	164	48.0	597	ABU49155	Abu49155 Protein e
18	163	47.7	599	ABU26544	Abu26544 Protein e
19	160	46.8	602	ABU41674	Abu41674 Protein e
20	159	46.5	602	ABU39826	Abu39826 Protein e
21	158.5	46.3	1157	AAU98050	Aau98050 Corynebac
22	158	46.2	100	AAR42120	Aar42120 Oxalaceta
23	158	46.2	607	ABU15742	Abu15742 Protein e
24	157	45.9	1146	ABBA47612	Abb47612 Listeria
25	157	45.9	1146	ABU32564	Abu32564 Protein e

ALIGNMENTS

RESULT 1

ABG72299
ID ABG72299 standard; protein; 70 AA.
XX
AC ABG72299;
XX
DT 21-MAR-2003 (first entry)
XX
DE Escherichia coli truncated PSTCD protein.
XX
KW Polypeptide labelling; biotinylation-competent fusion partner;
KW biotin acceptor peptide; BAP; virus; avidin; cell surface protein;
KW biotin ligase; BirA; drug therapy; Gene therapy targeting;
KW biotin labelled protein; P. shermanii transcarboxylase domain;
KW truncated PSTCD; mutant; mutein.
XX
OS Escherichia coli.
OS Synthetic.
XX
PN US2002142355-A1.
XX
PD 03-OCT-2002.
XX

PF 14-NOV-2001; 2001US-00987485.

PR 14-NOV-2000; 2000US-0247965P.

PA (BAYU) BAYLOR COLLEGE MEDICINE.

XX Barry MA, Parrott MB;

PI WPI; 2003-165810/16.

XX Novel fusion protein useful for targeting desired protein to cell in culture or in the body of subject, comprises biotinylation-competent protein/peptide, or biotin acceptor peptide (BAP), and desired polypeptide.

PS Claim 4; Fig 1; 13pp; English.

XX The present invention relates to methods for labelling polypeptides in mammalian cells with biotin. The methods involve expressing the protein joined to a biotinylation-competent fusion partner, or a biotin acceptor peptide (BAP). The fusion protein is useful for targeting a protein of interest which is on the surface of a virus, to a cell in culture, in the body of a subject. The method involves binding avidin to the surface of the cell, biotinylation of the fusion protein, where the protein of interest is joined to the biotinylation-competent protein or peptide, and

CC administering the biotinylated protein to either the medium surrounding
CC the cell in culture or to the subject. The protein of interest is used to
CC target the virus to the cell. A polynucleotide vector for expressing the
CC protein comprises a coding region consisting of nucleotides encoding a
CC fusion protein such as biotin ligase (e.g. BirA) directly linked to a
CC leader sequence (e.g. Iggappa secretory leader) is useful for
CC biotinylating a polypeptide of interest secreted by a mammalian host
CC cell. The fusion protein of the invention is useful for drug and gene
CC therapy targeting. The biotin labelled proteins are useful for delivering
CC nucleic acids to cell in vivo. The method is useful for rapidly purifying
CC a virus, for attaching other compounds to the virus, for modifying the
CC virus's ability to transduce cells in vivo and ex vivo, and for directing
CC the virus to specific avidin-tagged sites in a patient's body. The
CC present sequence represents Escherichia coli truncated PSTCD (P.
CC shermanii transcarboxylase domain) protein. Truncated PSTCD can be used
CC in a fusion protein of the invention

XX SQ Sequence 70 AA;

Query Match 100.0%; Score 342; DB 6; Length 70;
Best Local Similarity 100.0%; Pred. No. 3.5e-34;
Matches 70; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGEIPAPLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTGGKVEKLVKRDV 60
DB 1 EGEIPAPLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTGGKVEKLVKRDV 60

QY 61 QGGQGLIKIG 70
DB 61 QGGQGLIKIG 70

RESULT 2
ABG72298
ID ABG72298 standard; protein; 122 AA.
XX
AC ABG72298;
XX
DT 21-MAR-2003 (first entry)
XX
DE Escherichia coli full-length PSTCD protein.
XX
KW Polypeptide labelling; biotinylation-competent fusion partner;
KW biotin acceptor peptide; BAP; virus; avidin; cell surface protein;
KW biotin ligase; BirA; drug therapy; gene therapy targeting;
KW biotin labelled protein; P. shermanii transcarboxylase domain; PSTCD.
XX
OS Escherichia coli.
XX
PN US2002142355-A1.
XX
PD 03-OCT-2002.
XX
PF 14-NOV-2001; 2001US-00987485.
XX
PR 14-NOV-2000; 2000US-0247965P.
XX
PA (BAYU) BAYLOR COLLEGE MEDICINE.
XX
PI Barry MA, Parrott MB;
XX
DR WPI; 2003-165810/16.
XX
PT Novel fusion protein useful for targeting desired protein to cell in
PT culture or in the body of subject, comprises biotinylation-competent
PT protein/peptide, or biotin acceptor peptide (BAP), and desired
PT polypeptide.
XX
PS Claim 2; Fig 1; 13pp; English.
XX
CC The present invention relates to methods for labelling polypeptides in
CC mammalian cells with biotin. The methods involve expressing the protein
CC joined to a biotinylation-competent fusion partner, or a biotin acceptor

peptide (BAP). The fusion protein is useful for targeting a protein of
interest which is on the surface of a virus, to a cell in culture, in the
body of a subject. The method involves binding avidin to the surface of
the cell, biotinylation of the fusion protein, where the protein of
interest is joined to the biotinylation-competent protein or peptide, and
administering the biotinylated protein to either the medium surrounding
the cell in culture or to the subject. The protein of interest is used to
target the virus to the cell. A polynucleotide vector for expressing the
protein comprises a coding region consisting of nucleotides encoding a
fusion protein such as biotin ligase (e.g. BirA) directly linked to a
leader sequence (e.g. Iggappa secretory leader) is useful for
biotinylation a polypeptide of interest secreted by a mammalian host
cell. The fusion protein of the invention is useful for drug and gene
therapy targeting. The biotin labelled proteins are useful for delivering
nucleic acids to cell in vivo. The method is useful for rapidly purifying
a virus, for attaching other compounds to the virus, for modifying the
virus's ability to transduce cells in vivo and ex vivo, and for directing
the virus to specific avidin-tagged sites in a patient's body. The
present sequence represents Escherichia coli full-length PSTCD (P.
shermanii transcarboxylase domain) protein. PSTCD can be used in a fusion
protein of the invention

XX SQ Sequence 122 AA;

Query Match 100.0%; Score 342; DB 6; Length 122;
Best Local Similarity 100.0%; Pred. No. 7.2e-34;
Matches 70; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGEIPAPLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTGGKVEKLVKRDV 60
DB 53 EGEIPAPLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTGGKVEKLVKRDV 112

QY 61 QGGQGLIKIG 70
DB 113 QGGQGLIKIG 122

RESULT 3
AAR28177
ID AAR28177 standard; protein; 123 AA.
XX
AC AAR28177;
XX
DT 24-OCT-2003 (revised)
DT 25-MAR-2003 (revised)
DT 18-MAR-1993 (first entry)
XX
DE 1.3S polypeptide of Propionibacterium shermanii.
XX
KW avidin-binding; biotin; protein purification; affinity chromatography.
XX
OS Propionibacterium freudenreichii subsp. shermanii.
XX
FH Key Location/Qualifiers
FT Region 58..100
FT /label= biotin-binding_recognition_sequence
XX
PN EP511747-A1.
XX
PD 04-NOV-1992.
XX
PF 07-APR-1992; 92EP-00303067.
XX
PR 19-APR-1991; 91US-00687819.
XX
PA (ROHM) ROHM & HAAS CO.
XX
PI Cress DE, Haase FC;
XX
DR WPI; 1992-367575/45.
DR N-PSDB; AAQ29975.
XX
PT Hybrid polypeptide - contains a polypeptide fused to an avidin binding

PT polypeptide contg. a biotin attachment domain.

XX Claim 6; Page 23; 40pp; English.

PS The p.shermanii 1.3S polypeptide is a preferred avidin-binding

XX polypeptide for inclusion in the recombinant hybrid polypeptide of the

CC invention. In the hybrid, a polypeptide of interest is fused to the C-

CC terminus of the avidin-binding polypeptide. The hybrid polypeptide can

CC then be recovered in a single chromatographic step using avidin monomer

CC affinity chromatography. (Updated on 25-MAR-2003 to correct PN field.)

CC (Updated on 24-OCT-2003 to standardise OS field)

XX

SQ Sequence 123 AA;

Query Match 100.0%; Score 342; DB 2; Length 123;

Best Local Similarity 100.0%; Pred. No. 7.2e-34;

Matches 70; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGEIPAPLAGTVSKILVKEGDTVKGQTVLVLEAMKMETEINAPTQKVEKVLKRDV 60

Db 54 EGEIPAPLAGTVSKILVKEGDTVKGQTVLVLEAMKMETEINAPTQKVEKVLKRDV 113

QY 61 QGGQGLIKIG 70

Db 114 QGGQGLIKIG 123

RESULT 4

AAAY84002

ID AAY84002 standard; protein; 126 AA.

XX

AC AAY84002;

XX

DT 03-JUL-2000 (first entry)

XX

DE Amino acid sequence of a T. pallidum protein.

XX

KW Pinpoint vector; fusion protein antigen; membrane antigen; syphilis.

XX

OS Treponema pallidum.

XX

PN EP985931-A2. ✓

XX 15-MAR-2000.

XX

PF 12-AUG-1999; 99EP-00115877.

XX

PR 04-SEP-1998; 98US-00148920.

XX

PA (BECT) BECTON DICKINSON & CO.

XX

PI Mullenix MC, Deutsch J;

XX

DR WPI; 2000-226057/20.

DR N-PSDB; AAZ99247.

XX

PT Immunoassay for anti-Treponema pallidum antibodies, used for diagnosis of

PT syphilis using a fusion protein of membrane antigen with peptide sequence

PT that can be biotinylated in vivo.

XX

PS Disclosure; Page 12-13; 16pp; English.

XX

CC The present sequence represents a Treponema pallidum protein, which is

CC used to produce a fusion protein antigen for use in the method of the

CC invention. The specification describes a method for detecting antibodies

CC against Treponema pallidum. The antibodies are detected in a sample by

CC reaction with a fusion protein antigen, present in the mixture in

CC limiting concentration. The fusion protein antigen comprises a Treponema

CC pallidum membrane antigen. The method is used for diagnosis of syphilis

XX

SQ Sequence 126 AA;

Query Match 100.0%; Score 342; DB 3; Length 126;

Best Local Similarity 100.0%; Pred. No. 7.5e-34;

Matches 70; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGEIPAPLAGTVSKILVKEGDTVKGQTVLVLEAMKMETEINAPTQKVEKVLKRDV 60

Db 53 EGEIPAPLAGTVSKILVKEGDTVKGQTVLVLEAMKMETEINAPTQKVEKVLKRDV 112

QY 61 QGGQGLIKIG 70

Db 113 QGGQGLIKIG,122

RESULT 5

AAAY78908

ID AAY78908 standard; protein; 194 AA.

XX

AC AAY78908;

XX

DT 19-MAY-2000 (first entry)

XX

DE Outer surface protein C (OspC) DraI fragment amino acid sequence.

XX

KW Outer surface protein C; OspC; immunological epitope; Lyme disease;

KW vaccine; prevention; Borrelia infection; diagnose.

XX

OS Borrelia burgdorferi.

XX

PN WO200006745-A1.

XX 10-FEB-2000.

XX

PF 30-JUL-1999; 99WO-US017270.

XX

PR 31-JUL-1998; 98US-0094955P.

XX

PA (GUND-) GUNDERSEN LUTHERAN MEDICAL FOUND INC.

XX

PI Callister SN, Lovrich SD, Schell RF, Jobe DA;

XX

DR WPI; 2000-195305/17.

DR N-PSDB; AAZ92216.

XX

PT New immunogenic polypeptides useful as a vaccine against Lyme disease and

PT for treating and detecting borrelia infection in mammals consists an

PT epitope of Borrelia burgdorferi OspC fragment.

XX

PS Claim 3; Fig 4; 51pp; English.

XX

CC This sequence represents the Borrelia burgdorferi outer surface protein C

CC (OspC) DraI fragment amino acid sequence. The polypeptide contains an

CC immunological epitope used in the invention. Large amounts of OspC are

CC rapidly synthesised by B. burgdorferi shortly after attachment of

CC infected ticks to mammalian hosts. The OspC protein sequence is used to

CC diagnose B. borrelia infection in mammals. The OspC nucleotide sequence

CC is used to prevent (via vaccination), treat or detect Borrelia

CC (especially B. burgdorferi) infections, i.e. Lyme disease, in mammals

CC including humans. The OspC nucleotide sequence provides a superior

CC diagnostic antigen that detects early Lyme disease infection, predicts

CC successful eradication or the organism from the host, and discriminates

CC between individuals with Lyme disease and individuals who have been

CC vaccinated with an OspA Lyme disease vaccination. Detection of anti-OspC

CC borrelial antibodies advantageously gives an early diagnosis which

CC anti-OspA and anti-OspB borrelial antibodies cannot do. Unlike

CC vaccination with OspA, vaccination with OspC results in clearance of

CC spirochetes and resolution of symptoms even if administered after

CC infection with B. burgdorferi

XX

SQ Sequence 194 AA;

Query Match 100.0%; Score 342; DB 3; Length 194;

Best Local Similarity 100.0%; Pred. No. 1.3e-33;

Matches 70; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGEIPAPLAGTVSKILVKEGDTVKGQTVLVLEAMKMETEINAPTDGKVEKVLVKERDAV 60
Db 53 EGEIPAPLAGTVSKILVKEGDTVKGQTVLVLEAMKMETEINAPTDGKVEKVLVKERDAV 112
QY 61 QGGQGLIKIG 70
Db 113 QGGQGLIKIG 122

RESULT 6
AAW11886
ID AAW11886 standard; protein; 253 AA.
XX
AC AAW11886;
XX
DT 21-APR-1997 (first entry)
XX
DE Hantavirus nuclear protein sequence.
XX
KW Hantavirus nuclear protein; antigen; monoclonal antibody; diagnosis;
KW specificity.
XX
OS Hantavirus.
XX
PN JP08325291-A.
XX 10-DEC-1996.
XX
PF 30-MAY-1995; 95JP-00132460.
XX
PR 30-MAY-1995; 95JP-00132460.
XX
PA (ARIK/) ARIKAWA J.
PA (HASH/) HASHIMOTO N.
PA (ATAT-) A & T KK.
XX
DR WPI; 1997-083468/08.
XX
PT Hantavirus antigen protein and monoclonal antibody - used in the
PT diagnosis and treatment of hantavirus infection.
XX
PS Example 1; Page 17; 18pp; Japanese.
XX

102

CC The sequences given in AAW11872-86 represent Hantavirus nuclear proteins.
CC The N-terminal regions of these proteins may be used as antigens to raise
CC anti-hantavirus monoclonal antibodies. These antibodies are useful in
CC diagnosis of hantavirus infection due to their specificity to Hantavirus
XX
SQ Sequence 253 AA;

Query Match 100.0%; Score 342; DB 2; Length 253;
Best Local Similarity 100.0%; Pred. No. 1.9e-33;
Matches 70; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGEIPAPLAGTVSKILVKEGDTVKGQTVLVLEAMKMETEINAPTDGKVEKVLVKERDAV 60
Db 53 EGEIPAPLAGTVSKILVKEGDTVKGQTVLVLEAMKMETEINAPTDGKVEKVLVKERDAV 112
QY 61 QGGQGLIKIG 70
Db 113 QGGQGLIKIG 122

RESULT 7
AAW84001
ID AAY84001 standard; protein; 256 AA.
XX
AC AAY84001;
XX
DT 03-JUL-2000 (first entry)
XX
DE Amino acid sequence of a T. pallidum fusion protein antigen.
XX

KW PinPoint vector; fusion protein antigen; membrane antigen; syphilis.
XX
OS Synthetic.
OS Treponema pallidum.
XX
PN EP985931-A2.
XX
PD 15-MAR-2000.
XX
PF 12-AUG-1999; 99EP-00115877.
XX
PR 04-SEP-1998; 98US-00148920.
XX
PA (BECT) BECTON DICKINSON & CO.
XX
PI Mullenix MC, Deutsch J;
XX
DR WPI; 2000-226057/20.
DR N-PSDB; AAZ99246.
XX
PT Immunoassay for anti-Treponema pallidum antibodies, used for diagnosis of
PT syphilis using a fusion protein of membrane antigen with peptide sequence
PT that can be biotinylated in vivo.
XX
PS Claim 9; Page 10-11; 16pp; English.
XX
CC The present sequence represents a Treponema pallidum fusion protein
CC antigen. The protein is used in the method of the invention. The
CC specification describes a method for detecting antibodies against
CC Treponema pallidum. The antibodies are detected in a sample by reaction
CC with a fusion protein antigen, present in the mixture in limiting
CC concentration. The fusion protein antigen comprises a Treponema pallidum
CC membrane antigen. The method is used for diagnosis of syphilis
XX
SQ Sequence 256 AA;

Claim 9; Page 10-11; 16pp; English.

The present sequence represents a Treponema pallidum fusion protein antigen. The protein is used in the method of the invention. The specification describes a method for detecting antibodies against Treponema pallidum. The antibodies are detected in a sample by reaction with a fusion protein antigen, present in the mixture in limiting concentration. The fusion protein antigen comprises a Treponema pallidum membrane antigen. The method is used for diagnosis of syphilis

Query Match 100.0%; Score 342; DB 1; Length 256;
Best Local Similarity 100.0%; Pred. No. 1.9e-33;
Matches 70; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGEIPAPLAGTVSKILVKEGDTVKGQTVLVLEAMKMETEINAPTDGKVEKVLVKERDAV 60
Db 53 EGEIPAPLAGTVSKILVKEGDTVKGQTVLVLEAMKMETEINAPTDGKVEKVLVKERDAV 112
QY 61 QGGQGLIKIG 70
Db 113 QGGQGLIKIG 122

RESULT 8
AAW84003
ID AAY84003 standard; protein; 266 AA.
XX
AC AAY84003;
XX
DT 03-JUL-2000 (first entry)
XX
DE Amino acid sequence of a T. pallidum membrane protein antigen.
XX
KW PinPoint vector; fusion protein antigen; membrane antigen; syphilis.
XX
OS Treponema pallidum.
XX
PN EP985931-A2.
XX
PD 15-MAR-2000.
XX
PF 12-AUG-1999; 99EP-00115877.
XX
PR 04-SEP-1998; 98US-00148920.
XX
PA (BECT) BECTON DICKINSON & CO.

PI Mullenix MC, Deutsch J;
XX WPI; 2000-226057/20.
DR N-PSDB; AAZ99248.
XX
PT Immunoassay for anti-Treponema pallidum antibodies, used for diagnosis of
PT syphilis using a fusion protein of membrane antigen with peptide sequence
PT that can be biotinylated in vivo.
XX
PS Claim 9; Page 14-15; 16pp; English.
XX
CC The present sequence represents a Treponema pallidum membrane protein
CC antigen, which is used to produce a fusion protein antigen for use in the
CC method of the invention. The specification describes a method for
CC detecting antibodies against Treponema pallidum. The antibodies are
CC detected in a sample by reaction with a fusion protein antigen, present
CC in the mixture in limiting concentration. The fusion protein antigen
CC comprises a Treponema pallidum membrane antigen. The method is used for
CC diagnosis of syphilis
XX
SQ Sequence 266 AA;
Query Match 100.0%; Score 342; DB 3; Length 266;
Best Local Similarity 100.0%; Pred. No. 2e-33;
Matches 70; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EGEIPAPLAGTIVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKLVKXERDAV 60
Db 53 EGEIPAPLAGTIVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKLVKXERDAV 112
QY 61 QGGQGLIKIG 70
Db 113 QGGQGLIKIG 122
RESULT 9
AAU51122
ID AAU51122 standard; protein; 125 AA.
XX
AC AAU51122;
XX
DT 27-FEB-2002 (first entry)
XX
DE Propionibacterium acnes immunogenic protein #12018.
XX
KW SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis;
KW uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;
KW inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
KW dermatological; osteopathic; neuroprotectant.
XX
OS Propionibacterium acnes.
XX
PN WO200181581-A2.
XX
PD 01-NOV-2001.
XX
PF 20-APR-2001; 2001WO-US012865.
XX
PR 21-APR-2000; 2000US-0199047P.
PR 02-JUN-2000; 2000US-0208841P.
PR 07-JUL-2000; 2000US-0216747P.
XX
PA (CORI-) CORIXA CORP.
XX
PI Skeiky YAW, Persing DH, Mitcham JL, Wang SS, Bhatia A;
PI L'maisonneuve J, Zhang Y, Jen S, Carter D;
XX
DR WPI; 2001-616774/71.
DR N-PSDB; AAS59550.
XX
PT Propionibacterium acnes polypeptides and nucleic acids useful for
PT vaccinating against and diagnosing infections, especially useful for
PT treating acne vulgaris.

XX
PS Claim 6; SEQ ID NO 12317; 1069pp; English.
XX
CC Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic
CC polypeptides. The proteins and their associated DNA sequences are used in
CC the treatment, prevention and diagnosis of medical conditions caused by
CC P. acnes. The disorders include SAPHO syndrome (synovitis, acne,
CC pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis.
CC P. acnes is also involved in infections of bone, joints and the central
CC nervous system, however it is particularly involved in the inflammatory
CC lesions associated with acne vulgaris. A method for detecting the
CC presence or absence of P. acnes in a patient comprises contacting a
CC sample with a binding agent that binds to the proteins of the invention
CC and determining the amount of bound protein in the sample. The
CC polypeptides may be used as antigens in the production of antibodies
CC specific for P. acnes proteins. These antibodies can be used to
CC downregulate expression and activity of P. acnes polypeptides and
CC therefore treat P. acnes infections. The antibodies may also be used as
CC diagnostic agents for determining P. acnes presence, for example, by
CC enzyme linked immunosorbent assay (ELISA). Note: The sequence data for
CC this patent did not form part of the printed specification, but was
CC obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 125 AA;
Query Match 76.9%; Score 263; DB 4; Length 125;
Best Local Similarity 74.3%; Pred. No. 3.5e-24;
Matches 52; Conservative 7; Mismatches 11; Indels 0; Gaps 0;
QY 1 EGEIPAPLAGTIVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKLVKXERDAV 60
Db 56 EGEVPAPLAGTVAKILVAEGDAVKAGQVLLTLEAMKMETEINAPADGTVKILVAVGDAV 115
QY 61 QGGQGLIKIG 70
Db 116 QGGQGLVALG 125
RESULT 10
ABM47641
ID ABM47641 standard; protein; 125 AA.
XX
AC ABM47641;
XX
DT 20-OCT-2003 (first entry)
XX
DE Propionibacterium acnes immunogenic polypeptide #12317.
XX
KW Acne vulgaris; antiseborrheic; dermatological; antibacterial;
KW immunostimulant; immune response; vaccine; immunogenic.
XX
OS Propionibacterium acnes.
XX
PN WO2003033515-A1.
XX
PD 24-APR-2003.
XX
PF 11-OCT-2002; 2002WO-US032727.
XX
PR 15-OCT-2001; 2001US-00978825.
XX
PA (CORI-) CORIXA CORP.
XX
PI Mitcham JL, Skeiky YAW, Persing DH, Bhatia A, Maisonneuve JL;
PI Zhang Y, Wang S, Jen S, Lodes MJ, Benson DR, Jones R, Carter D;
PI Barth B, Vallieve-Douglas J;
XX
DR WPI; 2003-381789/36.
DR N-PSDB; ACF64479.
XX
PT New Propionibacterium acnes polypeptides and polynucleotides encoding the
PT polypeptide, useful for diagnosing, preventing or treating acne vulgaris,

PT or for stimulating an immune response specific for a P. acnes protein.
XX
PS Claim 6; SEQ ID NO 12317; 1481pp; English.
XX
CC The invention relates to an isolated polynucleotide (ACF64435-ACF64733)
CC encoding a Propionibacterium acnes protein. The invention also relates to
CC polypeptides encoded by the polynucleotides (ABM35624-ABM64536) and to
CC immunogenic fragments of P. acnes polypeptides. The invention
CC additionally encompasses expression vectors and host cells comprising a
CC polynucleotide of the invention; antibodies against polypeptides of the
CC invention; fusion proteins comprising a polypeptide of the invention; a
CC method for stimulating an immune response specific for a P. acnes
CC polypeptide and an isolated T cell population comprising T cells prepared
CC via this method; a vaccine composition (comprising P. acnes polypeptides,
CC polynucleotides, antibodies, fusion proteins, T cell populations, or
CC antigen-presenting cells that express the polypeptide); a method and kit
CC for detecting or determining the presence or absence of P. acnes in a
CC patient; and a method for inhibiting the development of P. acnes in a
CC patient. The P. acnes polypeptides, polynucleotides, antibodies, fusion
CC proteins, T cell populations or antigen-presenting cells that express the
CC polypeptides are useful for diagnosing, preventing or treating acne
CC vulgaris, or for stimulating an immune response specific for a P. acnes
CC protein. The polynucleotides can also be used as probes or primers for
CC nucleic acid hybridisation. The vaccine composition is useful for the
CC stimulation of an immune response against P. acnes, or for treating acne,
CC and the kit is useful for performing a diagnostic assay. The present
CC sequence represents a specifically claimed P. acnes polypeptide which is
CC thought to contain an immunogenic region. Note: The sequence data for
CC this patent did not form part of the printed specification, but was
CC obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 125 AA;

Query Match 76.9%; Score 263; DB 6; Length 125;
Best Local Similarity 74.3%; Pred. No. 3.5e-24;
Matches 52; Conservative 7; Mismatches 11; Indels 0; Gaps 0;
QY 1 EGEIPAPLAGTIVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTGGKVEKVLVKERDAV 60
DB 56 EGEVPAPLAGTIVAKILVAEGDAVKAGQVLLTLEAMKMETEINAPADGTGKILVAVGDAV 115
QY 61 QGGQGLIKIG 70
DB 116 QGGQGLVALG 125

RESULT 11
AAB96610
ID AAB96610 standard; protein; 148 AA.
XX
AC AAB96610;
XX
DT 29-OCT-2001 (first entry)
XX
DE Putative biotin carboxylase carrier protein of acetyl-CoA carboxylase.
XX
KW Hyperthermophilic archaeon; hyperthermophilic protein.
XX
OS Pyrococcus abyssi.
XX
PN FR2792651-A1.
XX
PD 27-OCT-2000.
XX
PF 21-APR-1999; 99FR-00005034.
XX
PF 21-APR-1999; 99FR-00005034.
XX
PR (CNRS) CNRS CENT NAT RECH SCI.
XX (IFRE-) IFREMER INST FR RECH EXPL MER.
PI Forterre P, Thierry JC, Prieur D, Dietrich J, Lecompte O;

PI Querellou J, Weissenbach J, Saurin W, Heilig R;
XX
DR WPI; 2001-126236/14.
XX
PT New nucleotide sequences isolated from Pyrococcus abyssi encode proteins
PT useful in industry.
XX
PS Claim 7; Page 1349; 1657pp; French.
XX
CC The present invention relates to the genomic sequence of Pyrococcus
CC abyssi (see AAF86431 and AAH41223-7) and P. abyssi proteins. P. abyssi is
CC a hyperthermophilic archaeon, which is isolated from deep-sea
CC hydrothermal vents. The present sequence is one such P. abyssi protein.
CC The proteins of the present invention have various potential industrial
CC uses, since the proteins are stable at very high temperatures, some up to
CC 110 degrees centigrade. Note: This patent is in the same patent family as
CC WO200065062, which contains additional sequences as shown in AAB99132-
CC AAB99143, AAH75903-AAH75920 and AAG66436
XX
SQ Sequence 148 AA;

Query Match 57.0%; Score 195; DB 4; Length 148;
Best Local Similarity 58.6%; Pred. No. 9.3e-16;
Matches 41; Conservative 10; Mismatches 19; Indels 0; Gaps 0;
QY 1 EGEIPAPLAGTIVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTGGKVEKVLVKERDAV 60
DB 79 ENVTAPMPGKVLKILVQEGQVQKLGQGLLILEAMKMETEINAPDRDGVVKRILVKEGDAV 138
QY 61 QGGQGLIKIG 70
DB 139 DTGTPLELG 148

RESULT 12
ABU18942
ID ABU18942 standard; protein; 1148 AA.
XX
AC ABU18942;
XX
DT 19-JUN-2003 (first entry)
XX
DE Protein encoded by Prokaryotic essential gene #4469.
XX
KW Antisense; prokaryotic essential gene; cell proliferation; drug design.
XX
OS Bacillus anthracis.
XX
PN WO200277183-A2.
XX
PD 03-OCT-2002.
XX
PF 21-MAR-2002; 2002WO-US009107.
XX
PR 21-MAR-2001; 2001US-00815242.
PR 06-SEP-2001; 2001US-00948993.
PR 25-OCT-2001; 2001US-0342923P.
PR 08-FEB-2002; 2002US-00072851.
PR 06-MAR-2002; 2002US-0362699P.
XX
PA (ELIT-) ELITRA PHARM INC.
XX
PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
XX
DR WPI; 2003-029926/02.
DR N-PSDB; ACA22812.
XX
PT New antisense nucleic acids, useful for identifying proteins or screening
PT for homologous nucleic acids required for cellular proliferation to
PT isolate candidate molecules for rational drug discovery programs.
XX
PS Claim 25; SEQ ID NO 46866; 1766pp; English.

XX The invention relates to an isolated nucleic acid comprising any one of
CC the 6213 antisense sequences given in the specification where expression
CC of the nucleic acid inhibits proliferation of a cell. Also included are:
CC (1) a vector comprising a promoter operably linked to the nucleic acid
CC encoding a polypeptide whose expression is inhibited by the antisense
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC polypeptide or its fragment whose expression is inhibited by the
CC antisense nucleic acid; (4) an antibody capable of specifically binding
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
CC proliferation or the activity of a gene in an operon required for
CC proliferation; (7) identifying a compound that influences the activity of
CC the gene product or that has an activity against a biological pathway
CC required for proliferation, or that inhibits cellular proliferation; (8)
CC identifying a gene required for cellular proliferation or the biological
CC pathway in which a proliferation-required gene or its gene product lies
CC or a gene on which the test compound that inhibits proliferation of an
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC compound's activity; (11) a culture comprising strains in which the gene
CC product is overexpressed or underexpressed; (12) determining the extent
CC to which each of the strains is present in a culture or collection of
CC strains; or (13) identifying the target of a compound that inhibits the
CC proliferation of an organism. The antisense nucleic acids are useful for
CC identifying proteins or screening for homologous nucleic acids required
CC for cellular proliferation to isolate candidate molecules for rational
CC drug discovery programs, or for screening homologous nucleic acids
CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of
CC the target prokaryotic essential genes. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 1148 AA;

Query Match 50.9%; Score 174; DB 6; Length 1148;
Best Local Similarity 53.0%; Pred. No. 5e-12;
Matches 35; Conservative 13; Mismatches 18; Indels 0; Gaps 0;

QY 4 IPAPLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTQKVEKVLVKERDAVQGG 63
DB 1081 ISATMPGTGVIKVVVKEGDEVKKGDSMAITEAMKMETTVQAPFNGKVKVYVNDGDAIQTG 1140

QY 64 QGLIKI 69
DB 1141 DLLIEL 1146

RESULT 13
ABU21035
ID ABU21035 standard; protein; 143 AA.
XX ABU21035;
XX
XX 19-JUN-2003 (first entry)
XX Protein encoded by Prokaryotic essential gene #6562.
DE Antisense; prokaryotic essential gene; cell proliferation; drug design.
XX Bacteroides fragilis.
XX
XX WO200277183-A2.
XX
XX 03-OCT-2002.
XX
XX 21-MAR-2002; 2002WO-US009107.
XX
XX 21-MAR-2001; 2001US-00815242.
PR 06-SEP-2001; 2001US-00948993.
PR 25-OCT-2001; 2001US-0342923P.
PR 08-FEB-2002; 2002US-00072851.
PR 06-MAR-2002; 2002US-0362699P.

XX (ELIT-) ELITRA PHARM INC.
XX PA Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
XX PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
XX WPI; 2003-029926/02.
DR N-PSDB; ACA24905.
XX New antisense nucleic acids, useful for identifying proteins or screening
PT for homologous nucleic acids required for cellular proliferation to
PT isolate candidate molecules for rational drug discovery programs.
XX Claim 25; SEQ ID NO 48959; 1766pp; English.
XX The invention relates to an isolated nucleic acid comprising any one of
CC the 6213 antisense sequences given in the specification where expression
CC of the nucleic acid inhibits proliferation of a cell. Also included are:
CC (1) a vector comprising a promoter operably linked to the nucleic acid
CC encoding a polypeptide whose expression is inhibited by the antisense
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC polypeptide or its fragment whose expression is inhibited by the
CC antisense nucleic acid; (4) an antibody capable of specifically binding
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
CC proliferation or the activity of a gene in an operon required for
CC proliferation; (7) identifying a compound that influences the activity of
CC the gene product or that has an activity against a biological pathway
CC required for proliferation, or that inhibits cellular proliferation; (8)
CC identifying a gene required for cellular proliferation or the biological
CC pathway in which a proliferation-required gene or its gene product lies
CC or a gene on which the test compound that inhibits proliferation of an
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC compound's activity; (11) a culture comprising strains in which the gene
CC product is overexpressed or underexpressed; (12) determining the extent
CC to which each of the strains is present in a culture or collection of
CC strains; or (13) identifying the target of a compound that inhibits the
CC proliferation of an organism. The antisense nucleic acids are useful for
CC identifying proteins or screening for homologous nucleic acids required
CC for cellular proliferation to isolate candidate molecules for rational
CC drug discovery programs, or for screening homologous nucleic acids
CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of
CC the target prokaryotic essential genes. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 143 AA;

Query Match 50.3%; Score 172; DB 6; Length 143;
Best Local Similarity 53.0%; Pred. No. 5.8e-13;
Matches 35; Conservative 11; Mismatches 20; Indels 0; Gaps 0;

QY 4 IPAPLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTQKVEKVLVKERDAVQGG 63
DB 77 VKSPLPGVILDIKVEGDTVKRGQTIILEAMKMENNINANKDGKVAEIKVKNKGSVLEG 136

QY 64 QGLIKI 69
DB 137 TDLVII 142

RESULT 14
ABU24164
ID ABU24164 standard; protein; 1144 AA.
XX ABU24164;
XX
XX 19-JUN-2003 (first entry)
XX Protein encoded by Prokaryotic essential gene #9691.
DE Antisense; prokaryotic essential gene; cell proliferation; drug design.
XX

XX OS Clostridium acetobutylicum.

XX PN WO200277183-A2.

XX PD 03-OCT-2002.

XX PF 21-MAR-2002; 2002WO-US009107.

XX PR 21-MAR-2001; 2001US-00815242.

XX PR 06-SEP-2001; 2001US-00948993.

XX PR 25-OCT-2001; 2001US-0342923P.

XX PR 08-FEB-2002; 2002US-00072851.

XX PR 06-MAR-2002; 2002US-0362699P.

XX PA (ELIT-) ELITRA PHARM INC.

XX PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;

XX PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;

XX DR WPI; 2003-029926/02.

XX DR N-PSDB; ACA28034.

XX PT New antisense nucleic acids, useful for identifying proteins or screening

XX PT for homologous nucleic acids required for cellular proliferation to

XX PT isolate candidate molecules for rational drug discovery programs.

XX PS Claim 25; SEQ ID NO 52088; 1766pp; English.

XX CC The invention relates to an isolated nucleic acid comprising any one of

XX CC the 6213 antisense sequences given in the specification where expression

XX CC of the nucleic acid inhibits proliferation of a cell. Also included are:

XX CC (1) a vector comprising a promoter operably linked to the nucleic acid

XX CC encoding a polypeptide whose expression is inhibited by the antisense

XX CC nucleic acid; (2) a host cell containing the vector; (3) an isolated

XX CC antisense nucleic acid; (4) an antibody capable of specifically binding

XX CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular

XX CC proliferation or the activity of a gene in an operon required for

XX CC proliferation; (7) identifying a compound that influences the activity of

XX CC the gene product or that has an activity against a biological pathway

XX CC required for proliferation, or that inhibits cellular proliferation; (8)

XX CC identifying a gene required for cellular proliferation or the biological

XX CC pathway in which a proliferation-required gene or its gene product lies

XX CC or a gene on which the test compound that inhibits proliferation of an

XX CC organism acts; (9) manufacturing an antibiotic; (10) profiling a

XX CC product is overexpressed or underexpressed; (12) determining the extent

XX CC to which each of the strains is present in a culture or collection of

XX CC strains; or (13) identifying the target of a compound that inhibits the

XX CC proliferation of an organism. The antisense nucleic acids are useful for

XX CC identifying proteins or screening for homologous nucleic acids required

XX CC for cellular proliferation to isolate candidate molecules for rational

XX CC drug discovery programs, or for screening homologous nucleic acids

XX CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,

XX CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of

XX CC the target prokaryotic essential genes. Note: The sequence data for this

XX CC patent did not form part of the printed specification, but was obtained

XX CC in electronic format directly from WIPO at

XX CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 1144 AA;

Query Match 48.8%; Score 167; DB 6; Length 1144;

Best Local Similarity 50.7%; Pred. No. 3.6e-11;

Matches 34; Conservative 11; Mismatches 22; Indels 0; Gaps 0;

QY 3 EIPAPLAGTVSKILVKGEDTVKAGQTVLVLEAMKMETEINAPTQKVEKVLVKERDAVQG 62

DB 1077 EIGASIPGNVVKVFPKDKVKKGDSLMVIEAMKMETNVSSEDGTGVGIFVKEGDQVQS 1136

QY 63 GQGLIKI 69

DB 1137 GQLLVKL 1143

RESULT 15

ABU33366

ID ABU33366 standard; protein; 596 AA.

XX AC ABU33366;

XX DT 19-JUN-2003 (first entry)

XX DE Protein encoded by Prokaryotic essential gene #18893.

XX KW Antisense; prokaryotic essential gene; cell proliferation; drug design.

XX OS Legionella pneumophila.

XX PN WO200277183-A2.

XX PD 03-OCT-2002.

XX PF 21-MAR-2002; 2002WO-US009107.

XX PR 21-MAR-2001; 2001US-00815242.

XX PR 06-SEP-2001; 2001US-00948993.

XX PR 25-OCT-2001; 2001US-0342923P.

XX PR 08-FEB-2002; 2002US-00072851.

XX PR 06-MAR-2002; 2002US-0362699P.

XX PA (ELIT-) ELITRA PHARM INC.

XX PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;

XX PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;

XX DR WPI; 2003-029926/02.

XX DR N-PSDB; ACA37236.

XX PT New antisense nucleic acids, useful for identifying proteins or screening

XX PT for homologous nucleic acids required for cellular proliferation to

XX PT isolate candidate molecules for rational drug discovery programs.

XX PS Claim 25; SEQ ID NO 61290; 1766pp; English.

XX CC The invention relates to an isolated nucleic acid comprising any one of

XX CC the 6213 antisense sequences given in the specification where expression

XX CC of the nucleic acid inhibits proliferation of a cell. Also included are:

XX CC (1) a vector comprising a promoter operably linked to the nucleic acid

XX CC encoding a polypeptide whose expression is inhibited by the antisense

XX CC nucleic acid; (2) a host cell containing the vector; (3) an isolated

XX CC polypeptide or its fragment whose expression is inhibited by the

XX CC antisense nucleic acid; (4) an antibody capable of specifically binding

XX CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular

XX CC proliferation or the activity of a gene in an operon required for

XX CC proliferation; (7) identifying a compound that influences the activity of

XX CC the gene product or that has an activity against a biological pathway

XX CC required for proliferation, or that inhibits cellular proliferation; (8)

XX CC identifying a gene required for cellular proliferation or the biological

XX CC pathway in which a proliferation-required gene or its gene product lies

XX CC or a gene on which the test compound that inhibits proliferation of an

XX CC organism acts; (9) manufacturing an antibiotic; (10) profiling a

XX CC product is overexpressed or underexpressed; (12) determining the extent

XX CC to which each of the strains is present in a culture or collection of

XX CC strains; or (13) identifying the target of a compound that inhibits the

XX CC proliferation of an organism. The antisense nucleic acids are useful for

XX CC identifying proteins or screening for homologous nucleic acids required

XX CC for cellular proliferation to isolate candidate molecules for rational

XX CC drug discovery programs, or for screening homologous nucleic acids

XX CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,

XX CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of

XX CC the target prokaryotic essential genes. Note: The sequence data for this

XX CC patent did not form part of the printed specification, but was obtained

XX CC in electronic format directly from WIPO at

XX CC ftp.wipo.int/pub/published_pct_sequences

CC of the nucleic acid inhibits proliferation of a cell. Also included are:
CC (1) a vector comprising a promoter operably linked to the nucleic acid
CC encoding a polypeptide whose expression is inhibited by the antisense
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC polypeptide or its fragment whose expression is inhibited by the
CC antisense nucleic acid; (4) an antibody capable of specifically binding
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
CC proliferation or the activity of a gene in an operon required for
CC proliferation; (7) identifying a compound that influences the activity of
CC the gene product or that has an activity against a biological pathway
CC required for proliferation, or that inhibits cellular proliferation; (8)
CC identifying a gene required for cellular proliferation or the biological
CC pathway in which a proliferation-required gene or its gene product lies
CC or a gene on which the test compound that inhibits proliferation of an
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC compound's activity; (11) a culture comprising strains in which the gene
CC product is overexpressed or underexpressed; (12) determining the extent
CC to which each of the strains is present in a culture or collection of
CC strains; or (13) identifying the target of a compound that inhibits the
CC proliferation of an organism. The antisense nucleic acids are useful for
CC identifying proteins or screening for homologous nucleic acids required
CC for cellular proliferation to isolate candidate molecules for rational
CC drug discovery programs, or for screening homologous nucleic acids
CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of
CC the target prokaryotic essential genes. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 597 AA;

Query Match 48.0%; Score 164; DB 6; Length 597;
Best Local Similarity 50.0%; Pred. No. 3.6e-11;
Matches 33; Conservative 14; Mismatches 19; Indels 0; Gaps 0;
QY 4 IPAPLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVLVKERDAVQGG 63
Db 531 VAAFLAGTIFKIQVEQGEVAEGDVLIVLEAMKMETEIRAARSGVIQELHVKEGDSVRVG 590
QY 64 QGLIKI 69
Db 591 ASLLSL 596

RESULT 18
ABU26544
ID ABU26544 standard; protein; 599 AA.
XX ABU26544;
AC
XX
XX
DT 19-JUN-2003 (first entry)
DE Protein encoded by Prokaryotic essential gene #12071.
XX Antisense; prokaryotic essential gene; cell proliferation; drug design.
KW Campylobacter jejuni.
XX
OS
XX
PN WO200277183-A2.
XX
PD 03-OCT-2002.
XX
PF 21-MAR-2002; 2002WO-US009107.
XX
PR 21-MAR-2001; 2001US-00815242.
PR 06-SEP-2001; 2001US-00948993.
PR 25-OCT-2001; 2001US-0342923P.
PR 08-FEB-2002; 2002US-00072851.
PR 06-MAR-2002; 2002US-0362699P.
XX
PA (ELIT-) ELITRA PHARM INC.
XX

PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
XX
DR WPI; 2003-029926/02.
XX N-PSDB; ACA30414.
PT New antisense nucleic acids, useful for identifying proteins or screening
PT for homologous nucleic acids required for cellular proliferation to
PT isolate candidate molecules for rational drug discovery programs.
XX
PS Claim 25; SEQ ID NO 54468; 1766pp; English.

CC The invention relates to an isolated nucleic acid comprising any one of
CC the 6213 antisense sequences given in the specification where expression
CC of the nucleic acid inhibits proliferation of a cell. Also included are:
CC (1) a vector comprising a promoter operably linked to the nucleic acid
CC encoding a polypeptide whose expression is inhibited by the antisense
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC polypeptide or its fragment whose expression is inhibited by the
CC antisense nucleic acid; (4) an antibody capable of specifically binding
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
CC proliferation or the activity of a gene in an operon required for
CC proliferation; (7) identifying a compound that influences the activity of
CC the gene product or that has an activity against a biological pathway
CC required for proliferation, or that inhibits cellular proliferation; (8)
CC identifying a gene required for cellular proliferation or the biological
CC pathway in which a proliferation-required gene or its gene product lies
CC or a gene on which the test compound that inhibits proliferation of an
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC compound's activity; (11) a culture comprising strains in which the gene
CC product is overexpressed or underexpressed; (12) determining the extent
CC to which each of the strains is present in a culture or collection of
CC strains; or (13) identifying the target of a compound that inhibits the
CC proliferation of an organism. The antisense nucleic acids are useful for
CC identifying proteins or screening for homologous nucleic acids required
CC for cellular proliferation to isolate candidate molecules for rational
CC drug discovery programs, or for screening homologous nucleic acids
CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of
CC the target prokaryotic essential genes. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 599 AA;

Query Match 47.7%; Score 163; DB 6; Length 599;
Best Local Similarity 50.0%; Pred. No. 4.7e-11;
Matches 33; Conservative 13; Mismatches 20; Indels 0; Gaps 0;
QY 1 EGEIPAPLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVLVKERDAV 60
Db 529 ENEVLAGISGNVFXIYVNEGEVKSQAIMVLEAMKMEIEVFNAPKDGIIELCIKIGDTV 588
QY 61 QGGQGL 66
Db 589 NEGEVL 594

RESULT 19
ABU41674
ID ABU41674 standard; protein; 602 AA.
XX
AC ABU41674;
XX
DT 19-JUN-2003 (first entry)
XX
DE Protein encoded by Prokaryotic essential gene #27201.
XX Antisense; prokaryotic essential gene; cell proliferation; drug design.
XX Pseudomonas syringae.
XX

strain, with feedback resistant pyruvate carboxylase gene through homologous recombination to form a second recombinant strain, where the homologous recombination in the above steps, occurs between the host cell and the vector. The feedback-resistant pyruvate carboxylase enzyme is resistant to feedback inhibition from aspartic acid. The present amino acid sequence represents the feedback-resistant pyruvate carboxylase enzyme of the invention

SQ	Sequence 1157 AA;
Query Match	46.3%; Score 158.5; DB 5; Length 1157;

QY 1 EGEIPAPLAGTIVSKILVKEGDTVVKAGQTVLVLEAMKMETEINAPTGDGKVEKVLVKERDAV 60

QY 61 QGGGLIKI 69
: || : :
1140 QGGGLIKI 1150

RESULT 22
AAR42120

XX

XX	05-MAY-1994	(first entry)
DT		
XX		
DE	Oxalacetate decarboxylase alpha subunit.	
XX		
KW	Fusion protein; post-translation modification; biotination; marker.	
XX		
OS	Klebsiella pneumoniae.	
XX		
PN	US5252466-A.	
XX		
PD	12-OCT-1993.	
XX		

XX
XX

XX

PA (UNII) UNIV ILLINOIS FOUND.

PI Cronan JE;

DR WPI; 1993-336075/42.

PT Fusion proteins having site for post-translation modification - utilised

xx
ps Claim 6; Page 57; 57pp; English.

The sequence is that of a portion of the alpha subunit of Klebsiella pneumoniae oxalacetate decarboxylase. It is used as part of a fusion protein allowing for post-translation biotination which provides a marker

CC identify the fusion protein or to isolate it from a mixt. of other

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XX      SQ      Sequence 100 AA;
          Query Match           46.2%; Score 158; DB 2; Length 100;
          Best Local Similarity 51.5%; Pred. No. 1.9e-11;
          Matches 34; Conservative 9; Mismatches 23; Indels 0; Gaps 0
QY      4 IPAPLAGTVSKILVKEGDTVKGQTIVLVLEAMKMETEINAPTGDGVKVKLVKERDAVQGG 63
          : ||||| : : | | | | | | | | | | | | | | | | | | | | | | | | | | | |

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Db 34 VTAPLAGFIWKVLASEGQTVAAAGEVLLILLEAMKMETEIRAAQAGTVRGIAVKAGDAVAVG 93

QY 64 QGLIKI 69

Db 94 DTLMTL 99

RESULT 23

ABU15742

ID ABU15742 standard; protein; 607 AA.

XX

AC ABU15742;

XX

DT 19-JUN-2003 (first entry)

XX

DE Protein encoded by prokaryotic essential gene #1269.

XX

KW Antisense; prokaryotic essential gene; cell proliferation; drug design.

XX

OS Pseudomonas aeruginosa.

XX

PN WO200277183-A2.

XX

PD 03-OCT-2002.

XX

PF 21-MAR-2002; 2002WO-US009107.

XX

PR 21-MAR-2001; 2001US-00815242.

PR 06-SEP-2001; 2001US-00948993.

PR 25-OCT-2001; 2001US-0342923P.

PR 08-FEB-2002; 2002US-00072851.

PR 06-MAR-2002; 2002US-0362699P.

XX

PA (ELIT-) ELITRA PHARM INC.

XX

PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;

PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;

XX

DR WPI; 2003-029926/02.

DR N-PSDB; ACA19612.

XX

PT New antisense nucleic acids, useful for identifying proteins or screening

PT for homologous nucleic acids required for cellular proliferation to

PT isolate candidate molecules for rational drug discovery programs.

XX

PS Claim 25; SEQ ID NO 43666; 1766pp; English.

XX

CC The invention relates to an isolated nucleic acid comprising any one of

CC the 6213 antisense sequences given in the specification where expression

CC of the nucleic acid inhibits proliferation of a cell. Also included are:

CC (1) a vector comprising a promoter operably linked to the nucleic acid

CC encoding a polypeptide whose expression is inhibited by the antisense

CC nucleic acid; (2) a host cell containing the vector; (3) an isolated

CC polypeptide or its fragment whose expression is inhibited by the

CC antisense nucleic acid; (4) an antibody capable of specifically binding

CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular

CC proliferation or the activity of a gene in an operon required for

CC proliferation; (7) identifying a compound that influences the activity of

CC the gene product or that has an activity against a biological pathway

CC required for proliferation, or that inhibits cellular proliferation; (8)

CC identifying a gene required for cellular proliferation or the biological

CC pathway in which a proliferation-required gene or its gene product lies

CC or a gene on which the test compound that inhibits proliferation of an

CC organism acts; (9) manufacturing an antibiotic; (10) profiling a

CC compound's activity; (11) a culture comprising strains in which the gene

CC product is overexpressed or underexpressed; (12) determining the extent

CC to which each of the strains is present in a culture or collection of

CC strains; or (13) identifying the target of a compound that inhibits the

CC proliferation of an organism. The antisense nucleic acids are useful for

CC identifying proteins or screening for homologous nucleic acids required

CC for cellular proliferation to isolate candidate molecules for rational

CC drug discovery programs, or for screening homologous nucleic acids

CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,

CC K. pneumoniae or *P. aeruginosa*. The present sequence is encoded by one of

CC the target prokaryotic essential genes. Note: The sequence data for this

CC patent did not form part of the printed specification, but was obtained

CC in electronic format directly from WIPO at

CC ftp.wipo.int/pub/published_pct_sequences

XX

SQ Sequence 607 AA;

Query Match 46.2%; Score 158; DB 6; Length 607;

Best Local Similarity 48.5%; Pred. No. 2e-10;

Matches 33; Conservative 12; Mismatches 23; Indels 0; Gaps 0;

QY 2 GEIPAPLAGTVSKILVKEGDTVKGQTVLVLEAMKMETEINAPTDCKVEKVLVKERDAVQ 61

Db 538 GHVSTTTPGNIVDVLVKEGDSVKAGQAVLITEAMKMETEVQAGIAGTVKAIHVAKGDRVN 597

QY 62 GGQGLIKI 69

Db 598 PGEILLIEI 605

RESULT 24

ABB47612

ID ABB47612 standard; protein; 1146 AA.

XX

AC ABB47612;

XX

DT 05-FEB-2002 (first entry)

XX

DE Listeria monocytogenes protein #316.

XX

KW Antibacterial; gene therapy; vaccine; biosynthesis; biodegradation;

KW vitamin B12; bacterial infection; disease.

XX

OS Listeria monocytogenes.

XX

PN WO200177335-A2.

XX

PD 18-OCT-2001.

XX

PF 11-APR-2001; 2001WO-FR001118.

XX

PR 11-APR-2000; 2000FR-00004629.

XX

PA (INSP) INST PASTEUR.

XX

PI Buchrieser C, Frangeul L, Couve E, Rusniok C, Fsihi H, Dehoux P;

PI Dussurget O, Chetouani F, Nedjari H, Glaser P, Kunst F, Cossart P;

PI Daniels J, Goebel W, Krefit J, Kuhn M, Ng E, Vazquez-Boland JA;

PI Dominguez-Bernal G, Garrido-Garcia P, Tierrez-Martinez A, Amend A;

PI Chakraborty T, Domann E, Hain T, Berche P, Charbit A, Durant L;

PI Perez-Diaz J, Baquero F, Garcia Del Portillo F, Gomez-Lopez N;

PI Maduenio E, De Pablos B, Wehland J, Kaerst U, Entian K, Hauf J;

PI Rose M, Voss H;

XX

DR WPI; 2002-010914/01.

XX

PT Genomic sequence for *Listeria monocytogenes*, useful e.g. for treatment

PT and prevention of *Listeria* and related bacterial infections, and related

PT polypeptides.

XX

PS Claim 6; SEQ ID NO 317; 192pp; French.

XX

CC The present invention relates to the genome sequence of *Listeria*

CC monocytogenes EGD-e (see ABA03041). The genome sequence and fragments of

CC it are useful for selecting probes and primers for detecting genes in *L.*

CC monocytogenes and related organisms, and for studying genetic

CC polymorphisms and other genomes. The present sequence is a protein

CC encoded by the genome sequence of the present invention. Proteins

CC expressed from the genome sequence are useful for raising specific

CC antibodies, identification of *L. monocytogenes* and related organisms, and

CC for biosynthesis and biodegradation, especially biosynthesis of Vitamin

CC B12. The genome sequence and proteins encoded by it are also useful for

CC selecting compounds that regulate gene expression and cell replication
CC and modulate L. monocytogenes-related diseases. In addition, the genome
CC sequence and proteins encoded by it are useful in pharmaceutical and
CC vaccines compositions for the treatment or prevention of infections by L.
CC monocytogenes and related organisms. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 1146 AA;

Query Match 45.9%; Score 157; DB 5; Length 1146;
Best Local Similarity 43.9%; Pred. No. 6e-10;
Matches 29; Conservative 17; Mismatches 20; Indels 0; Gaps 0;

QY 4 IPAPLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVLVKERDAVQGG 63
Db 1078 VGATMTGSGVIQVVVKGDSVKKGDPLLITEAMKMETTIQAPFDGEVSSIVSDGDTIESG 1137
QY 64 QGLIKI 69
Db 1138 DLLIEV 1143

RESULT 25
ABU32564
ID ABU32564 standard; protein; 1146 AA.
XX
AC ABU32564;
XX
DT 19-JUN-2003 (first entry)
XX
DE Protein encoded by Prokaryotic essential gene #18091.
XX
KW Antisense; prokaryotic essential gene; cell proliferation; drug design.
XX
OS Listeria monocytogenes.
XX
PN WO200277183-A2.
XX
PD 03-OCT-2002.
XX
PF 21-MAR-2002; 2002WO-US009107.
XX
PR 21-MAR-2001; 2001US-00815242.
PR 06-SEP-2001; 2001US-00948993.
PR 25-OCT-2001; 2001US-0342923P.
PR 08-FEB-2002; 2002US-00072851.
PR 06-MAR-2002; 2002US-0362699P.
XX
PA (ELIT-) ELITRA PHARM INC.
XX
PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
PI Wall D, Trawick JD, Carr GU, Yamamoto R, Forsyth RA, Xu HH;
XX
DR WPI; 2003-029926/02.
DR N-PSDB; ACA36434.
XX
XX New antisense nucleic acids, useful for identifying proteins or screening
PT for homologous nucleic acids required for cellular proliferation to
PT isolate candidate molecules for rational drug discovery programs.
XX
PS Claim 25; SEQ ID NO 60488; 1766pp; English.
XX
CC The invention relates to an isolated nucleic acid comprising any one of
CC the 6213 antisense sequences given in the specification where expression
CC of the nucleic acid inhibits proliferation of a cell. Also included are:
CC (1) a vector comprising a promoter operably linked to the nucleic acid
CC encoding a polypeptide whose expression is inhibited by the antisense
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC polypeptide or its fragment whose expression is inhibited by the
CC antisense nucleic acid; (4) an antibody capable of specifically binding
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular

CC proliferation or the activity of a gene in an operon required for
CC proliferation; (7) identifying a compound that influences the activity of
CC the gene product or that has an activity against a biological pathway
CC required for proliferation, or that inhibits cellular proliferation; (8)
CC identifying a gene required for cellular proliferation or the biological
CC pathway in which a proliferation-required gene or its gene product lies
CC or a gene on which the test compound that inhibits proliferation of an
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC compound's activity; (11) a culture comprising strains in which the gene
CC product is overexpressed or underexpressed; (12) determining the extent
CC to which each of the strains is present in a culture or collection of
CC strains; or (13) identifying the target of a compound that inhibits the
CC proliferation of an organism. The antisense nucleic acids are useful for
CC identifying proteins or screening for homologous nucleic acids required
CC for cellular proliferation to isolate candidate molecules for rational
CC drug discovery programs, or for screening homologous nucleic acids
CC required for proliferation in cells other than S. aureus, S. typhimurium,
CC K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of
CC the target prokaryotic essential genes. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 1146 AA;

Query Match 45.9%; Score 157; DB 6; Length 1146;
Best Local Similarity 43.9%; Pred. No. 6e-10;
Matches 29; Conservative 17; Mismatches 20; Indels 0; Gaps 0;

QY 4 IPAPLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVLVKERDAVQGG 63
Db 1078 VGATMTGSGVIQVVVKGDSVKKGDPLLITEAMKMETTIQAPFDGEVSSIVSDGDTIESG 1137
QY 64 QGLIKI 69
Db 1138 DLLIEV 1143

RESULT 26
AAB79298
ID AAB79298 standard; protein; 272 AA.
XX
AC AAB79298;
XX
DT 30-APR-2001 (first entry)
XX
DE Corynebacterium glutamicum SMP protein sequence SEQ ID NO:112.
XX
KW Corynebacterium glutamicum; carbon metabolism and energy production;
KW SMP protein; sugar metabolism and oxidative phosphorylation protein;
KW fine chemical production; organic acid; proteinogenic amino acid;
KW nonproteinogenic amino acid; purine base; pyrimidine base; nucleoside;
KW nucleotide; lipid; saturated fatty acid; unsaturated fatty acid; diol;
KW carbohydrate; aromatic compound; vitamin; cofactor; polypeptide; enzyme;
KW diagnosis; Corynebacterium diphtheriae; evolutionary study.
XX
OS Corynebacterium glutamicum.
XX
PN WO200100844-A2.
XX
PD 04-JAN-2001.
XX
PF 23-JUN-2000; 2000WO-IB000943.
XX
PR 25-JUN-1999; 99US-0141031P.
PR 08-JUL-1999; 99DE-01031412.
PR 08-JUL-1999; 99DE-01031413.
PR 08-JUL-1999; 99DE-01031419.
PR 08-JUL-1999; 99DE-01031420.
PR 08-JUL-1999; 99DE-01031424.
PR 08-JUL-1999; 99DE-01031428.
PR 08-JUL-1999; 99DE-01031431.
PR 08-JUL-1999; 99DE-01031433.

PR 08-JUL-1999; 99DE-01031434.
PR 08-JUL-1999; 99DE-01031510.
PR 08-JUL-1999; 99DE-01031562.
PR 08-JUL-1999; 99DE-01031634.
PR 09-JUL-1999; 99DE-01032180.
PR 09-JUL-1999; 99DE-01032227.
PR 09-JUL-1999; 99DE-01032230.
PR 09-JUL-1999; 99US-0143208P.
PR 14-JUL-1999; 99DE-01032924.
PR 14-JUL-1999; 99DE-01032973.
PR 14-JUL-1999; 99DE-01033005.
PR 27-AUG-1999; 99DE-01040765.
PR 31-AUG-1999; 99US-0151572P.
PR 03-SEP-1999; 99DE-01042076.
PR 03-SEP-1999; 99DE-01042086.
PR 03-SEP-1999; 99DE-01042087.
PR 03-SEP-1999; 99DE-01042088.
PR 03-SEP-1999; 99DE-01042095.
PR 03-SEP-1999; 99DE-01042123.
PR 03-SEP-1999; 99DE-01042125.
XX
PA (BADI) BASF AG.
XX
PI Pompejus M, Kroeger B, Schroeder H, Zelder O, Haberhauer G;
XX
DR WPI; 2001-061975/07.
DR N-PSDB; AAF71415.
XX
PT New isolated Corynebacterium glutamicum nucleic acid encoding a sugar
PT metabolism and oxidative phosphorylation protein for production or
PT modulation of production of fine chemicals e.g. amino acids,
PT carbohydrates or enzymes.
XX
PS Claim 20; Page 307-308; 1246pp; English.
XX
CC AAF71360 to AAF71750 encode the Corynebacterium glutamicum sugar
CC metabolism and oxidative phosphorylation (SMP) proteins given in AAB79243
CC to AAB 79633 which are involved in carbon metabolism and energy
CC production. The C. glutamicum SMP gene can be used in vectors (II) for
CC expression in host cells and production or modulation of production of
CC fine chemicals, such as, an organic acid, a proteinogenic or
CC nonproteinogenic amino acid (preferred), a purine or pyrimidine base, a
CC nucleoside, a nucleotide, a lipid, a saturated or unsaturated fatty acid,
CC a diol, a carbohydrate, an aromatic compound, a vitamin, a cofactor, a
CC polyketide, or an enzyme. The presence of (I) or SMP proteins (III)
CC encoded by them are used for diagnosing the presence or activity of
CC Corynebacterium diphtheriae in a subject. (I), (II), (III) or host cells
CC containing them are used to map genomes of organisms related to C.
CC glutamicum, identify and localise C. glutamicum sequences of interest, in
CC evolutionary studies, in determining SMP protein regions required for
CC function, in modulating SMP protein activity, in modulating the
CC metabolism of sugars, and in modulating high-energy molecule production
CC in a cell (i.e. ATP, NADPH)
XX
SQ Sequence 272 AA;
Query Match 45.5%; Score 155.5; DB 4; Length 272;
Best Local Similarity 44.9%; Pred. No. 1.4e-10;
Matches 31; Conservative 14; Mismatches 23; Indels 1; Gaps 1;
QY 1 EGEIPAPLAGTVSKILVKEGDTVKGQTVLVLEAMKMETEINAPTDGKVEKVLVKERDAV 60
Db 204 KGHVAAPFAGVVT-VTVAEGDEVKAGDAVAIIEMKMEATITASVDCKIDRVVVPAA TKV 262
QY 61 QGGQGLIKI 69
Db 263 EGGDLIVVV 271
RESULT 27
AAB79299
ID AAB79299 standard; protein; 272 AA.

XX AAB79299;
AC 30-APR-2001 (first entry)
XX
DT
DE Corynebacterium glutamicum SMP protein sequence SEQ ID NO:114.
XX
KW Corynebacterium glutamicum; carbon metabolism and energy production;
KW SMP protein; sugar metabolism and oxidative phosphorylation protein;
KW fine chemical production; organic acid; proteinogenic amino acid;
KW nonproteinogenic amino acid; purine base; pyrimidine base; nucleoside;
KW nucleotide; lipid; saturated fatty acid; unsaturated fatty acid; diol;
KW carbohydrate; aromatic compound; vitamin; cofactor; polyketide; enzyme;
KW diagnosis; Corynebacterium diphtheriae; evolutionary study.
XX
OS Corynebacterium glutamicum.
XX
PN WO200100844-A2.
XX
PD 04-JAN-2001.
XX
PF 23-JUN-2000; 2000WO-IB000943.
XX
PR 25-JUN-1999; 99US-0141031P.
PR 08-JUL-1999; 99DE-01031412.
PR 08-JUL-1999; 99DE-01031413.
PR 08-JUL-1999; 99DE-01031419.
PR 08-JUL-1999; 99DE-01031420.
PR 08-JUL-1999; 99DE-01031424.
PR 08-JUL-1999; 99DE-01031428.
PR 08-JUL-1999; 99DE-01031431.
PR 08-JUL-1999; 99DE-01031433.
PR 08-JUL-1999; 99DE-01031434.
PR 08-JUL-1999; 99DE-01031510.
PR 08-JUL-1999; 99DE-01031562.
PR 08-JUL-1999; 99DE-01031634.
PR 09-JUL-1999; 99DE-01032180.
PR 09-JUL-1999; 99DE-01032227.
PR 09-JUL-1999; 99DE-01032230.
PR 09-JUL-1999; 99US-0143208P.
PR 14-JUL-1999; 99DE-01032924.
PR 14-JUL-1999; 99DE-01032973.
PR 14-JUL-1999; 99DE-01033005.
PR 27-AUG-1999; 99DE-01040765.
PR 31-AUG-1999; 99US-0151572P.
PR 03-SEP-1999; 99DE-01042076.
PR 03-SEP-1999; 99DE-01042079.
PR 03-SEP-1999; 99DE-01042086.
PR 03-SEP-1999; 99DE-01042087.
PR 03-SEP-1999; 99DE-01042088.
PR 03-SEP-1999; 99DE-01042095.
PR 03-SEP-1999; 99DE-01042123.
PR 03-SEP-1999; 99DE-01042125.
XX
PA (BADI) BASF AG.
XX
PI Pompejus M, Kroeger B, Schroeder H, Zelder O, Haberhauer G;
XX
DR WPI; 2001-061975/07.
DR N-PSDB; AAF71416.
XX
PT New isolated Corynebacterium glutamicum nucleic acid encoding a sugar
PT metabolism and oxidative phosphorylation protein for production or
PT modulation of production of fine chemicals e.g. amino acids,
PT carbohydrates or enzymes.
XX
PS Claim 20; Page 310-311; 1246pp; English.
XX
CC AAF71360 to AAF71750 encode the Corynebacterium glutamicum sugar
CC metabolism and oxidative phosphorylation (SMP) proteins given in AAB79243
CC to AAB 79633 which are involved in carbon metabolism and energy
CC production. The C. glutamicum SMP gene can be used in vectors (II) for
CC expression in host cells and production or modulation of production of

XX Key Location/Qualifiers
FH Misc-difference 458
FT /note= "wild-type Pro substituted by Ser"
FT
XX EP1108790-A2.
XX PN
XX PD 20-JUN-2001.
XX PF 18-DEC-2000; 2000EP-00127688.
XX XX
PR 16-DEC-1999; 99JP-00377484.
PR 07-APR-2000; 2000JP-00159162.
PR 03-AUG-2000; 2000JP-00280988.
XX XX
PA (KYOW) KYOWA HAKKO KOGYO KK.
XX XX
PI Nakagawa S, Mizoguchi H, Ando S, Hayashi M, Ochiai K, Yokoi H;
PI Tateishi N, Senoh A, Ikeda M, Ozaki A;
XX XX
DR WPI; 2001-376931/40.
XX XX
PT Novel polynucleotides derived from Coryneform bacteria, for identifying
PT mutation point of a gene, measuring expression of a gene, analyzing
PT expression profile or pattern of a gene and identifying homologous gene.
XX XX
PS Claim 43; Page; 246pp + Sequence Listing; English.
PS XX
CC The present invention provides a number of nucleotide and protein
CC sequences from the Coryneform bacterium Corynebacterium glutamicum. These
CC are useful for identifying the mutation point of a gene derived from a
CC mutant of coryneform bacterium, measuring expression amount and analysing
CC the expression profile or expression pattern of a gene derived from
CC Coryneform bacterium, and identifying a homologue of a gene derived from
CC coryneform bacterium. Coryneform bacteria are useful for producing amino
CC acids, nucleic acids, vitamins, saccharides and organic acids,
CC particularly L-lysine. The present sequence is a mutant protein described
CC in the exemplification of the invention. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from the European Patent Office
XX XX
SQ Sequence 1140 AA;
Query Match 45.5%; Score 155.5; DB 4; Length 1140;
Best Local Similarity 44.9%; Pred. No. 9.1e-10;
Matches 31; Conservative 14; Mismatches 23; Indels 1; Gaps 1;
QY 1 EGEIPAPLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTQKVEKVLVKERDAV 60
Db 1072 KGHVAAPFAGVVT-VTVAEDEVKAGDAVAIIIEAMKMEATITASVDGKIDRVVVPAAATKV 1130
QY 61 QGGQGLIKI 69
Db 1131 EGGDLIVV 1139
RESULT 33
AAE25601
ID AAE25601 standard; protein; 1140 AA.
XX AC AAE25601;
XX DT 04-NOV-2002 (first entry)
XX XX
DE Corynebacterium glutamicum pyruvate carboxylase protein.
XX XX
KW Pyruvate carboxylase; anaplerotic enzyme; industrial fermentation;
XX KW oxaloacetate; growth; enzyme.
XX OS Corynebacterium glutamicum.
XX XX
FH Key Location/Qualifiers
FT Misc-difference 1

FT XX
XX US6403351-B1.
XX PN
XX PD 11-JUN-2002.
XX XX
XX PF 03-OCT-2000; 2000US-00677575.
XX PF 23-DEC-1998; 98US-00220081.
XX PR (ARCH) ARCHER-DANIELS MIDLAND CO.
XX PA
XX PI Sinskey AJ, Lessard PA, Willis LB;
XX XX
DR WPI; 2002-536037/57.
DR N-PSDB; AAD42046.
XX XX
PT Novel pyruvate carboxylase polypeptide, useful for replenishing
PT oxaloacetate consumed for biosynthesis during growth, or lysine and
PT glutamic acid production in industrial fermentation.
XX XX
PS Claim 1; Col 29-36; 28pp; English.
XX XX
CC The present invention relates to novel pyruvate carboxylase proteins and
CC polynucleotides encoding such proteins. Sequences of the invention are
CC important anaplerotic enzymes for replenishing oxaloacetate consumed for
CC biosynthesis during growth, or lysine and glutamic acid production in
CC industrial fermentation. The present sequence is C. glutamicum pyruvate
CC carboxylase protein
XX XX
SQ Sequence 1140 AA;
Query Match 45.5%; Score 155.5; DB 5; Length 1140;
Best Local Similarity 44.9%; Pred. No. 9.1e-10;
Matches 31; Conservative 14; Mismatches 23; Indels 1; Gaps 1;
QY 1 EGEIPAPLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTQKVEKVLVKERDAV 60
Db 1072 KGHVAAPFAGVVT-VTVAEDEVKAGDAVAIIIEAMKMEATITASVDGKIDRVVVPAAATKV 1130
QY 61 QGGQGLIKI 69
Db 1131 EGGDLIVV 1139
RESULT 34
AAU98053
ID AAU98053 standard; protein; 1140 AA.
XX AC AAU98053;
XX DT 27-AUG-2002 (first entry)
XX XX
DE Corynebacterium wild-type feedback-resistant pyruvate carboxylase enzyme.
XX XX
KW Feedback-resistant; pyruvate carboxylase; enzyme;
KW aspartic acid feedback inhibition resistant.
XX OS Corynebacterium glutamicum.
XX XX
PN WO200231158-A2.
XX PD 18-APR-2002.
XX XX
PF 12-OCT-2001; 2001WO-US031893.
XX PF 13-OCT-2000; 2000US-0239913P.
XX PR (ARCH) ARCHER-DANIELS MIDLAND CO.
XX PA
XX PI Hanke PD;
XX XX
DR WPI; 2002-463267/49.

Novel mutated, feedback resistant pyruvate carboxylase enzyme polypeptide, useful for producing amino acids e.g. L-lysine, L-threonine, L-glycine, L-glutamic acid, L-proline and L-methionine and L-isoleucine.

Disclosure; Fig 2; 42pp; English.

The present invention relates to a new mutated, feedback-resistant pyruvate carboxylase enzyme. The invention is useful for producing an amino acid (e.g. L-Lys, L-Thr, L-Met, L-Ile, L-Glu, L-Arg and L-Pro), by culturing a host cell in a suitable media and separating the amino acid from the medium. The vector of the invention is useful for replacement of a wild-type pyruvate carboxylase gene, with a feedback resistant pyruvate carboxylase gene, in a *Corynebacterium glutamicum*, by replacing a genomic copy of the wild-type pyruvate carboxylase gene with a selectable marker gene through homologous recombination to form a first recombinant strain, and replacing the selectable marker gene in the first recombinant strain, with feedback resistant pyruvate carboxylase gene through homologous recombination to form a second recombinant strain, where the homologous recombination in the above steps, occurs between the host cell and the vector. The feedback-resistant pyruvate carboxylase enzyme is resistant to feedback inhibition from aspartic acid. The present amino acid sequence represents the wild-type feedback-resistant pyruvate carboxylase enzyme of the invention

Sequence 1140 AA;

PT anaplerotic enzyme replenishing oxaloacetate consumed for biosynthesis
PT during growth, or for lysine or glutamic acid production in industrial
PT fermentations.
XX
PS Claim 1; Page 16-19; 29pp; English.
XX
CC The invention describes a new isolated pyruvate carboxylase polypeptide
CC having an amino acid sequence at least 95% identical to a sequence
CC comprising 1140 amino acids from *Corynebacterium glutamicum*, or the
CC complete amino acid sequence encoded by the cosmid clone deposited with
CC the American Type Culture Collection. The polypeptide is useful as an
CC anaplerotic enzyme replenishing oxaloacetate consumed for biosynthesis
CC during growth. The polypeptide is also useful for lysine or glutamic acid
CC production in industrial fermentations. This is the amino acid sequence
CC of *Corynebacterium glutamicum* pyruvate carboxylase
XX
SQ Sequence 1140 AA;

Query Match 45.5%; Score 155.5; DB 7; Length 1140;
Best Local Similarity 44.9%; Pred. No. 9.1e-10;
Matches 31; Conservative 14; Mismatches 23; Indels 1; Gaps 1;

QY 1 EGEIPAPLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTQKVEKVLVKERDAV 60
Db 1072 KGHVAAPFAGVVT-VTVAEGDEVKAGDAVAIIIEAMKMEATITASVDGKIDRVVVVPAATKV 1130
:
QY 61 QGGQGLIKI 69
:
Db 1131 EGGDLIVV 1139
:

RESULT 36
AAB01436
ID AAB01436 standard; protein; 1141 AA.
XX AAB01436;
XX
DT 20-OCT-2000 (first entry)
DE Pyruvate carboxylase of *C. glutamicum*.
XX
KW Pyruvate carboxylase; expression; amino acid biosynthesis; lysine;
KW glutamic acid; oxaloacetate; fermentation; biosynthesis.
XX
OS *Corynebacterium glutamicum*.
XX
PN WO200039305-A1.
XX
PD 06-JUL-2000.
XX
PF 23-DEC-1998; 98WO-US027301.
XX
PR 23-DEC-1998; 98WO-US027301.
XX
PA (SINS/) SINSKEY A J.
PA (LESS/) LESSARD P A.
PA (WILL/) WILLIS L B.
XX
PI Sinskey AJ, Lessard PA, Willis LB;
XX
XX WPI; 2000-465746/40.
DR N-PSDB; AAA47533.
XX
PT Novel polynucleotides encoding *Corynebacterium glutamicum* pyruvate
PT carboxylase useful for industrial fermentation processes comprises a
PT specific nucleotide sequence.
XX
PS Claim 3; Fig 1; 51pp; English.
XX
CC The pyruvate carboxylase of *Corynebacterium glutamicum* can be used for
CC producing amino acids, preferably lysine and glutamic acid in industrial
CC fermentations and for replenishing oxaloacetate consumed for biosynthesis
CC during growth. By incorporating the pyruvate carboxylase gene in

CC expression vectors levels of expression can be 2 - 20 fold higher than in

CC Corynebacterium glutamicum

XX Sequence 1141 AA;

SQ

Query Match 45.5%; Score 155.5; DB 3; Length 1141;

Best Local Similarity 44.9%; Pred. No. 9.1e-10;

Matches 31; Conservative 14; Mismatches 23; Indels 1; Gaps 1;

QY 1 EGEIPAPLAGTIVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTQDGKVEKVLVKERDAV 60

Db 1073 KGHVAAPFAGVVT-VTVAEGDEVKAGDAVAIIEMKMEATITASVDGKIDRVVVPAATKV 1131

QY 61 QGGQGLIKI 69

Db 1132 EGGDLIVVV 1140

RESULT 37

ABU25961

ID ABU25961 standard; protein; 1141 AA.

XX

AC ABU25961;

XX

DT 19-JUN-2003 (first entry)

XX

DE Protein encoded by Prokaryotic essential gene #11488.

XX

KW Antisense; prokaryotic essential gene; cell proliferation; drug design.

XX

OS Corynebacterium diphtheriae.

XX

PN WO200277183-A2.

XX

PD 03-OCT-2002.

XX

PF 21-MAR-2002; 2002WO-US009107.

XX

PR 21-MAR-2001; 2001US-00815242.

PR

PR 06-SEP-2001; 2001US-00948993.

PR

PR 25-OCT-2001; 2001US-0342923P.

PR

PR 08-FEB-2002; 2002US-00072851.

PR

PR 06-MAR-2002; 2002US-0362699P.

XX

XX (ELIT-) ELITRA PHARM INC.

XX

PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;

PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;

XX

DR WPI; 2003-029926/02.

DR

DR N-PSDB; ACA29831.

XX

XX New antisense nucleic acids, useful for identifying proteins or screening

PT for homologous nucleic acids required for cellular proliferation to

PT isolate candidate molecules for rational drug discovery programs.

XX

PS Claim 25; SEQ ID NO 53885; 1766pp; English.

XX

CC The invention relates to an isolated nucleic acid comprising any one of

CC the 6213 antisense sequences given in the specification where expression

CC of the nucleic acid inhibits proliferation of a cell. Also included are:

CC (1) a vector comprising a promoter operably linked to the nucleic acid

CC encoding a polypeptide whose expression is inhibited by the antisense

CC nucleic acid; (2) a host cell containing the vector; (3) an isolated

CC polypeptide or its fragment whose expression is inhibited by the

CC antisense nucleic acid; (4) an antibody capable of specifically binding

CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular

CC proliferation or the activity of a gene in an operon required for

CC proliferation; (7) identifying a compound that influences the activity of

CC the gene product or that has an activity against a biological pathway

CC required for proliferation, or that inhibits cellular proliferation; (8)

CC identifying a gene required for cellular proliferation or the biological

CC pathway in which a proliferation-required gene or its gene product lies

or a gene on which the test compound that inhibits proliferation of an

organism acts; (9) manufacturing an antibiotic; (10) profiling a

compound's activity; (11) a culture comprising strains in which the gene

product is overexpressed or underexpressed; (12) determining the extent

to which each of the strains is present in a culture or collection of

strains; or (13) identifying the target of a compound that inhibits the

proliferation of an organism. The antisense nucleic acids are useful for

identifying proteins or screening for homologous nucleic acids required

for cellular proliferation to isolate candidate molecules for rational

drug discovery programs, or for screening homologous nucleic acids

required for proliferation in cells other than S. aureus, S. typhimurium,

K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of

the target prokaryotic essential genes. Note: The sequence data for this

patent did not form part of the printed specification, but was obtained

in electronic format directly from WIPO at

ftp.wipo.int/pub/published_pct_sequences

Query Match 45.5%; Score 155.5; DB 6; Length 1141;

Best Local Similarity 47.1%; Pred. No. 9.1e-10;

Matches 32; Conservative 15; Mismatches 20; Indels 1; Gaps 1;

QY 2 GEIPAPLAGTIVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTQDGKVEKVLVKERDAVQ 61

Db 1074 GHVAAPFAGVVT-VTIEEGATVKAGDPVAVIEAMKMEATISATDGTVDRLVTQATKVE 1132

QY 62 GGQGLIKI 69

Db 1133 GGDLLVI 1140

RESULT 38

ABU24853

ID ABU24853 standard; protein; 1144 AA.

XX

AC ABU24853;

XX

DT 19-JUN-2003 (first entry)

XX

DE Protein encoded by Prokaryotic essential gene #10380.

XX

KW Antisense; prokaryotic essential gene; cell proliferation; drug design.

XX

OS Clostridium botulinum.

XX

PN WO200277183-A2.

XX

PD 03-OCT-2002.

XX

PF 21-MAR-2002; 2002WO-US009107.

XX

PR 21-MAR-2001; 2001US-00815242.

PR

PR 06-SEP-2001; 2001US-00948993.

PR

PR 25-OCT-2001; 2001US-0342923P.

PR

PR 08-FEB-2002; 2002US-00072851.

PR

PR 06-MAR-2002; 2002US-0362699P.

XX

XX (ELIT-) ELITRA PHARM INC.

XX

PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;

PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;

XX

DR WPI; 2003-029926/02.

DR

DR N-PSDB; ACA28723.

XX

XX New antisense nucleic acids, useful for identifying proteins or screening

PT for homologous nucleic acids required for cellular proliferation to

PT isolate candidate molecules for rational drug discovery programs.

XX

PS Claim 25; SEQ ID NO 52777; 1766pp; English.

XX

CC The invention relates to an isolated nucleic acid comprising any one of

CC the 6213 antisense sequences given in the specification where expression
CC of the nucleic acid inhibits proliferation of a cell. Also included are:
CC (1) a vector comprising a promoter operably linked to the nucleic acid
CC encoding a polypeptide whose expression is inhibited by the antisense
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC polypeptide or its fragment whose expression is inhibited by the
CC antisense nucleic acid; (4) an antibody capable of specifically binding
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
CC proliferation; (7) identifying a compound that influences the activity of
CC the gene product or that has an activity against a biological pathway
CC required for proliferation, or that inhibits cellular proliferation; (8)
CC identifying a gene required for cellular proliferation or the biological
CC pathway in which a proliferation-required gene or its gene product lies
CC or a gene on which the test compound that inhibits proliferation of an
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC compound's activity; (11) a culture comprising strains in which the gene
CC product is overexpressed or underexpressed; (12) determining the extent
CC to which each of the strains is present in a culture or collection of
CC strains; or (13) identifying the target of a compound that inhibits the
CC proliferation of an organism. The antisense nucleic acids are useful for
CC identifying proteins or screening for homologous nucleic acids required
CC for cellular proliferation to isolate candidate molecules for rational
CC drug discovery programs, or for screening homologous nucleic acids
CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of
CC the target prokaryotic essential genes. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 1144 AA;

Query Match 44.7%; Score 153; DB 6; Length 1144;
Best Local Similarity 48.5%; Pred. No. 1.8e-09;
Matches 32; Conservative 14; Mismatches 20; Indels 0; Gaps 0;

OY 4 IPAPLAGTIVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTQKVEKVLVKERDAVQGG 63
Db 1078 IGSSIPGTIVKLVNKGDEIKEGDSLIVIEAMKMETNIVASLSGVVGSLLVKEGDQVKS 1137

OY 64 QGLIKI 69
Db 1138 QLLLEL 1143

RESULT 39
AAU98052
ID AAU98052 standard; protein; 1140 AA.

XX AAU98052;
XX 27-AUG-2002 (first entry)

XX Corynebacterium mutant feedback-resistant pyruvate carboxylase enzyme.

DE Feedback-resistant; pyruvate carboxylase; enzyme;
XX aspartic acid feedback inhibition resistant; mutant; mutein.

XX Corynebacterium glutamicum.
OS Synthetic.

XX Key Location/Qualifiers
FH Misc-difference 1 /note= "Wild-type Met substituted by Val"
FT Misc-difference 153
FT Misc-difference 182 /note= "Wild-type Glu substituted by Asp"
FT Misc-difference 182 /note= "Wild-type Ala substituted by Ser"
FT Misc-difference 206 /note= "Wild-type Ala substituted by Ser"
FT Misc-difference 227 /note= "Wild-type His substituted by Arg"

FT Misc-difference 455 /note= "Wild-type Ala substituted by Gly"
FT Region 1110. .1122
FT /note= "Specifically claimed in claim 18"
FT Misc-difference 1116
FT /note= "Wild-type Asp substituted by Glu"

XX WO200231158-A2.

PN 18-APR-2002.

XX 12-OCT-2001; 2001WO-US031893.

XX 13-OCT-2000; 2000US-0239913P.

PA (ARCH) ARCHER-DANIELS MIDLAND CO.

PI Hanke PD;

XX WPI; 2002-463267/49.

XX Novel mutated, feedback resistant pyruvate carboxylase enzyme
PT polypeptide, useful for producing amino acids e.g. L-lysine, L-threonine,
PT L-glycine, L-glutamic acid, L-proline and L-methionine and L-isoleucine.

XX Claim 1; Page; 42pp; English.

XX The present invention relates to a new mutated, feedback-resistant
CC pyruvate carboxylase enzyme. The invention is useful for producing an
CC amino acid (e.g. L-Lys, L-Thr, L-Met, L-Ile, L-Glu, L-Arg and L-Pro), by
CC culturing a host cell in a suitable media and separating the amino acid
CC from the medium. The vector of the invention is useful for replacement of
CC a wild-type pyruvate carboxylase gene, with a feedback resistant pyruvate
CC carboxylase gene, in a Corynebacterium glutamicum, by replacing a genomic
CC copy of the wild-type pyruvate carboxylase gene with a selectable marker
CC gene through homologous recombination to form a first recombinant
CC strain, and replacing the selectable marker gene in the first recombinant
CC strain, with feedback resistant pyruvate carboxylase gene through
CC homologous recombination to form a second recombinant strain, where the
CC homologous recombination in the above steps, occurs between the host cell
CC and the vector. The feedback-resistant pyruvate carboxylase enzyme is
CC resistant to feedback inhibition from aspartic acid. The present amino
CC acid sequence represents the mutant feedback-resistant pyruvate
CC carboxylase enzyme of the invention. Note: The present sequence is not
CC shown in the specification but is derived from the wild-type feedback-
CC resistant pyruvate carboxylase enzyme (AAU98053) given in figure 2 of the
CC specification

XX Sequence 1140 AA;

Query Match 44.3%; Score 151.5; DB 5; Length 1140;
Best Local Similarity 43.5%; Pred. No. 2.8e-09;
Matches 30; Conservative 15; Mismatches 23; Indels 1; Gaps 1;

OY 1 EGEIPAPLAGTIVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTQKVEKVLVKERDAV 60
Db 1072 KGHVAAPFAGVVT-VTVAEGDEVKAGDAVAIEAMKMEATITASVEGKIDRVVVPAAATKV 1130

OY 61 QGGQGLIKI 69
Db 1131 EGGDLIVVV 1139

RESULT 40
ABP28014
ID ABP28014 standard; protein; 166 AA.

XX ABP28014;

XX 02-JUL-2002 (first entry)

XX Streptococcus polypeptide SEQ ID NO 5204.

KW Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae;
KW group A streptococcus; Streptococcus pyogenes; antibacterial;
KW antiinflammatory; infection; vaccine; meningitis; gene therapy.
XX
OS Streptococcus pyogenes.
XX
PN WO200234771-A2.
XX
PD 02-MAY-2002.
XX
PF 29-OCT-2001; 2001WO-GB004789.
XX
PR 27-OCT-2000; 2000GB-00026333.
PR 24-NOV-2000; 2000GB-00028727.
PR 07-MAR-2001; 2001GB-00005640.
XX
PA (CHIR-) CHIRON SPA.
PA (GENO-) INST GENOMIC RES.
XX
PI Telford J, Massignani V, Margarit Y RosI, Grandi G, Fraser C;
PI Tettelin H;
XX
DR WPI; 2002-352536/38.
DR N-PSDB; ABN68645.
XX
PT New Streptococcus protein for the treatment or prevention of infection or
PT disease caused by Streptococcus bacteria, such as meningitis, and for
PT detecting a compound that binds to the protein.
XX
PS Claim 1; Page 3684; 4525pp; English.
XX
CC The invention relates to a protein (ABP25413-ABP30895) from group B
CC streptococcus/GAS (Streptococcus agalactiae) or group A streptococcus/GAS
CC (Streptococcus pyogenes), comprising one of 5483 sequences (S1), given in
CC the specification. The proteins have antibacterial and antiinflammatory
CC activity. (I), nucleic acids encoding (I), ABN6044-ABN71526 and
CC antibodies that bind (I) are used in the manufacture of medicaments for
CC the treatment or prevention of infection or disease caused by
CC Streptococcus bacteria, particularly S. agalactiae and S. pyogenes.
CC Nucleic acids encoding (I) are used to detect Streptococcus in a
CC biological sample. (I) is used to determine whether a compound binds to
CC (I). A composition comprising (I) or a nucleic acid encoding (I), may be
CC used as a vaccine or diagnostic composition. The disease caused by
CC Streptococcus that is prevented or treated may be meningitis. Nucleic
CC acid encoding (I) may be used to recombinantly produce (I) and may be
CC used in gene therapy. Antibodies to (I) are used for affinity
CC chromatography, immunoassays, and distinguishing/identifying
CC Streptococcus proteins
XX
SQ Sequence 166 AA;

Query Match		44.2%	Score 151;	DB 5;	Length 166;
Best Local Similarity		41.6%	Pred. No. 2.6e-10;		
Matches	32;	Conservative	15;	Mismatches	22;
				Indels	8;
				Gaps	2;
Qy	1	EGEI-PAPLAGTV-----SKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKV	52		
Db	89	EGDIVESPLVGVAAYLAASPKPPFVAVGDTVKKGQTLVILEAMKVMNEVPAPCDGVITEI	148		
Qy	53	LVKERDAVQGGGLIKI	69		
Db	149	LVSNEDEVIEFGGLVRI	165		

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OM protein - protein search, using sw model

Run on: March 3, 2004, 10:26:14 ; Search time 17.7917 Seconds
(without alignments)
659.599 Million cell updates/sec

Title: US-09-987-485A-1
Perfect score: 615
Sequence: 1 MKLKVTVNGTAYDVDVDK.....KVLVKERDAVQGGQLIKIG 122

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_78:*
1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	604.5	98.3	123	1 BKIP	biotin carboxyl ca
2	231.5	37.6	145	2 F75135	methylmalonyl-coa
3	221	35.9	149	2 A71074	probable methylmal
4	205	33.3	129	2 D49094	methylmalonyl-CoA
5	200.5	32.6	596	2 A28088	oxaloacetate decar
6	198.5	32.3	134	2 T44984	methylmalonyl-CoA
7	190.5	31.0	655	2 B70432	pyruvate carboxyla
8	190	30.9	140	2 H69526	methylmalonyl-CoA
9	187.5	30.5	599	2 D81367	probable pyruvate
10	185	30.1	597	2 G82308	oxaloacetate decar
11	184	29.9	571	2 F71133	probable oxaloacet
12	176.5	28.7	576	2 AC3038	biotin carboxylase
13	176.5	28.7	576	2 H98247	biotin carboxylase
14	176	28.6	134	2 C72341	propionyl-CoA carb
15	176	28.6	984	2 T44608	pyruvate carboxyla
16	175.5	28.5	591	2 B44465	sodium ion pump ox
17	175.5	28.5	610	2 G84306	biotin carboxylase
18	173.5	28.2	186	2 D90418	hypothetical prote
19	173.5	28.2	591	2 AB0509	oxaloacetate decar
20	173.5	28.2	591	2 AE0909	oxaloacetate decar
21	173	28.1	567	2 F64453	oxaloacetate decar
22	170	27.6	1144	2 D97227	pyruvate carboxyla
23	168.5	27.4	607	2 F82966	probable transcarb
24	168.5	27.4	620	2 F70439	oxaloacetate decar
25	166	27.0	600	2 F70980	probable accA3 pro
26	165	26.8	1150	2 A83978	pyruvate carboxyla
27	164	26.7	654	2 G87517	acetyl/propionyl-C
28	163	26.5	142	2 D69510	oxaloacetate decar
29	163	26.5	598	2 G86999	hypothetical prote

30	163	26.5	598	2 A55579	biotin carboxyl ca
31	162	26.3	591	2 S71009	biotin carboxylase
32	162	26.3	597	2 S71006	biotin carboxylase
33	161.5	26.3	1174	2 AE2911	pyruvate carboxyla
34	161.5	26.3	1174	2 C97686	pyruvate carboxyla
35	159	25.9	665	2 G97819	hypothetical prote
36	158.5	25.8	593	2 B71373	probable oxaloacet
37	157	25.5	161	2 A95049	hypothetical prote
38	157	25.5	161	2 G97919	acetyl-CoA carboxy
39	157	25.5	170	2 F87482	hypothetical prote
40	157	25.5	1146	2 AC1565	pyruvate carboxyla
41	157	25.5	1146	2 AH1208	pyruvate carboxyla
42	156	25.4	1150	2 G89881	pyruvate carboxyla
43	155	25.2	167	2 T44291	biotin carboxyl ca
44	153.5	25.0	436	2 A53568	methylcrotonoyl-Co
45	152.5	24.8	162	2 A97521	biotin carboxyl ca

ALIGNMENTS

RESULT 1

BKIP

biotin carboxyl carrier protein [validated] - Propionibacterium freudenreichii subsp. s.
N;Alternate names: methylmalonyl-CoA carboxyltransferase biotin carboxyl carrier protei
C;Species: Propionibacterium freudenreichii subsp. shermanii
C;Date: 31-Mar-1980 #sequence_revision 31-Mar-1980 #text_change 01-Feb-2002
C;Accession: A03401

R;Maloy, W.L.; Bowien, B.U.; Zwolinski, G.K.; Kumar, K.G.; Wood, H.G.; Ericsson, L.H.;
J. Biol. Chem. 254, 11615-11622, 1979
A;Title: Amino acid sequence of the biotinyl subunit from transcarboxylase.
A;Reference number: A03401; MUID:80049796; PMID:40985

A;Accession: A03401

A;Molecule type: protein

A;Residues: 1-123 <MAL>

C;Comment: Six or 12 chains of biotin carboxyl carrier protein (BCCP) are found in the
onyl coenzyme A to BCCP and (2) from BCCP to pyruvate, forming oxalacetate.
C;Comment: See PIR:A48665 and PIR:S36808.

C;Superfamily: biotin carboxyl carrier protein; lipoyl/biotin-binding homology
C;Keywords: biotin binding
F;50-123/Domain: lipoyl/biotin-binding homology <LPB>

F;89/Binding site: biotin (Lys) (covalent) #status experimental

Query Match 98.3%; Score 604.5; DB 1; Length 123;
Best Local Similarity 99.2%; Pred. No. 2.7e-41;
Matches 122; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 MKLKVTVNGTAYDVDVDKSHENPMGTILFGGTTGGAPAP-AAGGAGAGKAGEGEIPAP 59

Db 1 MKLKVTVNGTAYDVDVDKSHENPMGTILFGGTTGGAPAPRAAGGAGAGKAGEGEIPAP 60

QY 60 LAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVLVKERDAVQGGQLI 119

Db 61 LAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVLVKERDAVQGGQLI 120

QY 120 KIG 122

Db 121 KIG 123

RESULT 2

F75135

methylmalonyl-coa decarboxylase gamma chain PAB1771 - Pyrococcus abyssi (strain Orsay)
C;Species: Pyrococcus abyssi

C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000

C;Accession: F75135

R;anonymous, Genoscope

submitted to the EMBL Data Library, July 1999

A;Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome str
A;Reference number: A75001

A;Accession: F75135

A;Status: preliminary

A;Molecule type: DNA


```
RESULT 10
GB2308
oxaloacetate decarboxylase, alpha chain VC0550 [similarity] - Vibrio cholerae (strain N1
C;Species: Vibrio cholerae
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
C;Accession: G82308
R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;
chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, P
l, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; MUID:20406833; PMID:10952301
A;Accession: G82308
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-597 <HEI>
A;Cross-references: GB:AE004141; GB:AE003852; NID:99654976; PIDN:AAF93718.1; GSPDB:GN001
A;Experimental source: serogroup O1; strain N16961; biotype El Tor
C;Genetics:
A;Gene: VC0550
A;Map position: 1
C;Superfamily: Klebsiella pneumoniae oxaloacetate decarboxylase alpha chain; lipoyl/biot
Query Match 30.1%; Score 185; DB 2; Length 597;
Best Local Similarity 39.3%; Pred. No. 2.4e-07;
Matches 46; Conservative 18; Mismatches 45; Indels 8; Gaps 2;
QY 5 VTVNGTAYDVDVDKSHENPMGTILFGGGTGGAPAPAGGAGAGKAGEGEIPAPLAGTV 64
Db 488 VKVDGVVYDVEV-----GSQGQLTSVVPAGQKAAPKLAATPTQGAEA-VAAPLAGTI 539
QY 65 SKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVLVKERDAVQGGQGLIKI 121
Db 540 PKIQVEQGDEVAEGDVLIVLEAMKMETEIRAARSGVIOELHVKEGDSVRVGASLLSL 596
RESULT 11
F71133
probable oxaloacetate decarboxylase alpha chain - Pyrococcus horikoshii
C;Species: Pyrococcus horikoshii
C;Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 18-Aug-2000
C;Accession: F71133
R;Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Sekin
M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi
DNA Res. 5, 55-76, 1998
A;Title: Complete sequence and gene organization of the genome of a hyper-thermophilic a
A;Reference number: A71000; MUID:98344137; PMID:9679194
A;Accession: F71133
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-571 <KAW>
A;Cross-references: GB:AP000003; NID:G3236130; PIDN:BA29928.1; PID:G3257245
A;Experimental source: strain OT3
A;Note: this accession replaces an interim accession for a sequence replaced by GenBank
C;Genetics:
A;Gene: PH0834
C;Superfamily: Klebsiella pneumoniae oxaloacetate decarboxylase alpha chain; lipoyl/biot
F;498-571/Domain: lipoyl/biotin-binding homology <LPB>
F;537/Binding site: biotin (Lys) (covalent) #status predicted
Query Match 29.9%; Score 184; DB 2; Length 571;
Best Local Similarity 37.5%; Pred. No. 2.7e-07;
Matches 45; Conservative 24; Mismatches 43; Indels 8; Gaps 3;
QY 3 LKVTVNGTAYDVDVD-VDKSHENPMGTILFGGGTGGAPAPAGGAGAGKAGEGEIPAPLA 61
Db 458 IKIYINGKEFEVFEVGEIEFEPKPKQV---QAIPSQPPKREVAPSGSV----VSAEMP 510
QY 62 GTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVLVKERDAVQGGQGLIKI 121
Db 511 GKVLRLVVRGDRVRVGQGLLVLEAMKMEINEIPSRDGVVVKRLVKEGEAVDTGQPLIEL 570
```

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RESULT 12
AC3038
biotin carboxylase [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
C;Accession: AC3038
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo,
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kuttyavin, T.; Levy, R.; Li, M.; McCle
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm
ster, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; MUID:21608550; PMID:11743193
A;Accession: AC3038
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-576 <KUR>
A;Cross-references: GB:AE008689; PIDN:AAL44721.1; PID:gl7742353; GSPDB:GN00187
A;Experimental source: strain C58 (Dupont)
C;Genetics:
A;Gene: Atu3913
A;Map position: linear chromosome
C;Superfamily: propionyl-CoA carboxylase alpha chain; biotin carboxylase homology; lip
Query Match 28.7%; Score 176.5; DB 2; Length 576;
Best Local Similarity 43.8%; Pred. No. 1.1e-06;
Matches 42; Conservative 17; Mismatches 28; Indels 9; Gaps 3;
QY 26 MGTILFGGGTGGAPAPAGGAGAGKAGEGEIPAPLAGTVSKILVKEGDTVKAGQTVLVLE 85
Db 488 LGTV--SGGNASAPSAV-----EKKEGEMTAPVSGTLQSFVKVDGETVSEGDLLAVME 539
QY 86 AMKMETEINAPTDGKVEKVLVKERDAVQGGQGLIKI 121
Db 540 AMKMETQIVATRAGKV-RLIVKEG DYLOAGATLIDI 574
```

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RESULT 13
H98247
biotin carboxylase protein A2 [imported] - Agrobacterium tumefaciens (strain C58, Cere
C;Species: Agrobacterium tumefaciens
C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 18-Nov-2002
C;Accession: H98247
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Quorollo, B.; Goldma
A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B
Science 294, 2323-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium ti
A;Reference number: A97359; MUID:21608551; PMID:11743194
A;Accession: H98247
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-576 <KUR>
A;Cross-references: GB:AE007870; PIDN:AAK89506.1; PID:gl5159380; GSPDB:GN00170
C;Genetics:
A;Gene: AGR_L1864
A;Map position: linear chromosome
C;Superfamily: propionyl-CoA carboxylase alpha chain; biotin carboxylase homology; lip
Query Match 28.7%; Score 176.5; DB 2; Length 576;
Best Local Similarity 43.8%; Pred. No. 1.1e-06;
Matches 42; Conservative 17; Mismatches 28; Indels 9; Gaps 3;
QY 26 MGTILFGGGTGGAPAPAGGAGAGKAGEGEIPAPLAGTVSKILVKEGDTVKAGQTVLVLE 85
Db 488 LGTV--SGGNASAPSAV-----EKKEGEMTAPVSGTLQSFVKVDGETVSEGDLLAVME 539
QY 86 AMKMETEINAPTDGKVEKVLVKERDAVQGGQGLIKI 121
Db 540 AMKMETQIVATRAGKV-RLIVKEG DYLOAGATLIDI 574
```

RESULT 14
C72341
propionyl-CoA carboxylase, gamma subunit - Thermotoga maritima (strain MSB8)
C:Species: Thermotoga maritima
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C:Accession: C72341
R:Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.
C.M.
Nature 399, 323-329, 1999
A:Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq
A:Reference number: A72200; MUID:99287316; PMID:10360571
A:Accession: C72341
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-134 <ARN>
A:Cross-references: GB:AE001743; GB:AE000512; NID:g4981241; PIDN:AAD35799.1; PID:g498124
A:Experimental source: strain MSB8
C:Genetics:
A:Gene: TM0717
C:Superfamily: biotin carboxyl carrier protein; lipoyl/biotin-binding homology

Query Match 28.6%; Score 176; DB 2; Length 134;
Best Local Similarity 33.6%; Pred. No. 2.8e-07;
Matches 49; Conservative 18; Mismatches 37; Indels 42; Gaps 4;

QY 2 KLKVTVNGTAYDVVDV---VDKSH-----ENPMGTILFGGTGGA 38
DB 4 KFRVVNGKEYIVEEIGNVRKKEPAEKPAKVSQKTVEIPKEPKPVVL----- 55

QY 39 PAPAAGGAGAGKAGEGE---IPAPLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINA 95
DB 56 -----EREKSSDQEEKLVKAPMAGIVLVKVEGQKVVGVGDKLLVFEAMKVENELQS 107

QY 96 PTDGKVEKVLVKERDAVQGGGLIKI 121
DB 108 EFGSGTVKEILVKEGDNIEGTQILMKI 133

RESULT 15
T44608
pyruvate carboxylase (EC 6.4.1.1) [imported] - Bacillus cereus (fragment)
C:Species: Bacillus cereus
C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 02-Sep-2000
C:Accession: T44608
R:Okstad, O.A.; Hegna, I.; Lindbaeck, T.; Rishovd, A.L.; Kolsto, A.B.
Microbiology 145, 621-631, 1999
A:Title: Genome organisation is not conserved between Bacillus cereus and Bacillus subtil
A:Reference number: Z22811; MUID:99231848; PMID:10217496
A:Accession: T44608
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-984 <OKS>
A:Cross-references: EMBL:AJ010111; NID:g4584147; PIDN:CAB40604.1; PID:g4584148
A:Experimental source: ATCC 10987
C:Genetics:
A:Note: pycA
C:Superfamily: pyruvate carboxylase; biotin carboxylase homology; lipoyl/biotin-binding
C:Keywords: ligase

Query Match 28.6%; Score 176; DB 2; Length 984;
Best Local Similarity 33.8%; Pred. No. 2e-06;
Matches 45; Conservative 19; Mismatches 49; Indels 20; Gaps 2;

QY 9 GTAYDVVDVVDKS-----HENPMGTILFGGTGGAP-----APAGGAGA 48
DB 850 GEEIDVEIEQKTLMKVLVSGEPQPDGNNRVLYLEFNGQPREIVVKDESVKATVAQRVKG 909

QY 49 GKAGEGHPAPLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVLVKE 108
DB 910 NRENPNHISATMPGTVIKVVVKEGDEVKKGDSMAITEAMKMETTVQAPFNGKVKVYVND 969

QY 109 RDAVQGGQGLIKI 121
DB 970 GDAIQTGDLIEL 982

RESULT 16
B44465
sodium ion pump oxaloacetate decarboxylase subunit alpha - Salmonella typhimurium
C:Species: Salmonella typhimurium
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 18-Aug-2000
C:Accession: B44465
R:Woehlke, G.; Wifling, K.; Dimroth, P.
J. Biol. Chem. 267, 22798-22803, 1992
A:Title: Sequence of the sodium ion pump oxaloacetate decarboxylase from Salmonella typh
A:Reference number: A44465; MUID:93054591; PMID:1331067
A:Accession: B44465
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-591 <WOE>
A:Cross-references: GB:M96434; NID:g154195; PIDN:AAA02973.1; PID:g408892
A:Experimental source: LT2
A:Note: sequence extracted from NCBI backbone
C:Superfamily: Klebsiella pneumoniae oxaloacetate decarboxylase alpha chain; lipoyl/bio
F:518-591/Domain: lipoyl/biotin-binding homology <LPB>
F:557/Binding site: biotin (Lys) (covalent) #status predicted

Query Match 28.5%; Score 175.5; DB 2; Length 591;
Best Local Similarity 37.5%; Pred. No. 1.3e-06;
Matches 48; Conservative 10; Mismatches 41; Indels 29; Gaps 3;

QY 5 VTVNGTAYDVVDVVDKSHENPMGTILFGGG-----TGAPAPAAAGGAGAGKAGE 53
DB 481 VEVEGKAFVVKVS-----DGGDISQLTAAPVPAASSAPVQAAAPAGAGT--- 523

QY 54 GEIPAPLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVLVKERDAVQ 113
DB 524 -PVTAPLAGNIWKVIATEGQTVAEQDVLILEAMKMETEIRAAQAGTVRGIAVKSQDAVS 582

QY 114 GQGGGLIKI 121
DB 583 VGDTLMTL 590

RESULT 17
G84306
biotin carboxylase [imported] - Halobacterium sp. NRC-1
C:Species: Halobacterium sp. NRC-1
C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001
C:Accession: G84306
R:Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S
; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jabl
Jung, K.H.; Alam, M.; Freitas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A:Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; L
A:Title: Genome sequence of Halobacterium species NRC-1.
A:Reference number: A84160; MUID:20504483; PMID:11016950
A:Accession: G84306
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-610 <STO>
A:Cross-references: GB:AE004437; NID:g10581019; PIDN:AAG19819.1; GSPDB:GN00138
C:Genetics:
A:Gene: acc
C:Superfamily: propionyl-CoA carboxylase alpha chain; biotin carboxylase homology; lipo

Query Match 28.5%; Score 175.5; DB 2; Length 610;
Best Local Similarity 38.1%; Pred. No. 1.4e-06;
Matches 48; Conservative 18; Mismatches 43; Indels 17; Gaps 5;

QY 5 VTVNGTAYDVVDVVDKSHENPMGTILFGG-----GTGAPAPAAAGGAGAGKA---GEGE- 55
DB 492 VEVNGKRFEVNL-----ERGAQAFAAPEADTGGGPPPEP-ACGADDGETVVEGDGET 543

```
QY 56 IPAPLAGTVSKILVKEGDTVKGQTVLVLEAMKMETEINAPTDGKVEKVLVKERDAVQGG 115
Db 544 VTAEMQGTILDVAVSEGDVADAGDVLVLEAMKMNENDVVAASHGGTVTQVAVSEDDSDMD 603

QY 116 QGLIKI 121
Db 604 DVLVVI 609

RESULT 18
D90418
hypothetical protein SSO2464 [imported] - Sulfolobus solfataricus
C:Species: Sulfolobus solfataricus
C>Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 24-May-2001
C:Accession: D90418
R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-
Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, H
arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
submitted to GenBank, April 2001
A:Description: Sulfolobus solfataricus complete genome.
A:Reference number: A99139
A:Accession: D90418
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-186 <KUR>
A:Cross-references: GB:AE006641; NID:G13815767; PIDN:AAK42603.1; GSPDB:GN00155
C:Genetics:
A:Gene: SSO2464

Query Match 28.2%; Score 173.5; DB 2; Length 186;
Best Local Similarity 40.0%; Pred. No. 6.1e-07;
Matches 50; Conservative 14; Mismatches 42; Indels 19; Gaps 4;

QY 7 VNGTAYDVDVDKSHENPMGTILFGG-----TGGAPAPAGGAGA----GKAGEGEI 56
Db 70 INGKKYYVFIESD-----GTLIFNHQDFLRDKVTEIPKGEHVEEIRGK--EGEI 120

QY 57 PAPLAGTVSKILVKEGDTVKGQTVLVLEAMKMETEINAPTDGKVEKVLVKERDAVQGGQ 116
Db 121 VSPFLGRVVKIRVKEGDVAVKNGQPLLSIEAMKAETVISSPIGGIVQKILIKEGGQVKKGD 180

QY 117 GLIKI 121
Db 181 ILIVI 185

RESULT 19
AB0509
oxaloacetate decarboxylase (EC 4.1.1.3) alpha chain [imported] - Salmonella enterica sub
C:Species: Salmonella enterica subsp. enterica serovar Typhi
A:Note: this species has also been called Salmonella typhi
C>Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C:Accession: AB0509
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
th, T.; Connerton, P.; Cronin, A.; Davies, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
A:Reference number: AB0502; MUID:21534947; PMID:11677608
A:Accession: AB0509
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-591 <PAR>
A:Cross-references: GB:AL513382; PIDN:CAD01210.1; PID:G16501339; GSPDB:GN00176
C:Genetics:
A:Gene: oada
C:Superfamily: Klebsiella pneumoniae oxaloacetate decarboxylase alpha chain; lipoyl/bio
C:Keywords: carbon-carbon lyase; carboxy-lyase

Query Match 28.2%; Score 173.5; DB 2; Length 591;
Best Local Similarity 40.2%; Pred. No. 1.9e-06;
Matches 47; Conservative 14; Mismatches 49; Indels 7; Gaps 3;
```

```
QY 5 VTVNGTAYDVDVDKSHENPMGTILFGGTTGGAPAPAGGAGAGKAGEGEIPAPLAGTV 64
Db 481 VEVEGKAFVVRVS-DGGDISQLTTAV--PAASSAPVQAAAPAGAGT-----PVTAPLAGNI 533

QY 65 SKILVKEGDTVKGQTVLVLEAMKMETEINAPTDGKVEKVLVKERDAVQGGQGLIKI 121
Db 534 WKVIATEGQSVAEAGDVLVLEAMKMETEIRAAQAAGTVRGIAVKSQDAVSVGDTLMTL 590

RESULT 20
AE0909
oxaloacetate decarboxylase (EC 4.1.1.3) alpha chain [imported] - Salmonella enterica su
C:Species: Salmonella enterica subsp. enterica serovar Typhi
A:Note: this species has also been called Salmonella typhi
C>Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C:Accession: AE0909
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher
th, T.; Connerton, P.; Cronin, A.; Davies, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar
, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.
A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serc
A:Reference number: AB0502; MUID:21534947; PMID:11677608
A:Accession: AE0909
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-591 <PAR>
A:Cross-references: GB:AL513382; PIDN:CAD07867.1; PID:G16504414; GSPDB:GN00176
C:Genetics:
A:Gene: oada
C:Superfamily: Klebsiella pneumoniae oxaloacetate decarboxylase alpha chain; lipoyl/bio
C:Keywords: carbon-carbon lyase; carboxy-lyase

Query Match 28.2%; Score 173.5; DB 2; Length 591;
Best Local Similarity 40.2%; Pred. No. 1.9e-06;
Matches 47; Conservative 14; Mismatches 49; Indels 7; Gaps 3;

QY 5 VTVNGTAYDVDVDKSHENPMGTILFGGTTGGAPAPAGGAGAGKAGEGEIPAPLAGTV 64
Db 481 VEVEGKAFVVRVS-DGGDISQLTTAV--PAASSAPVQAAAPAGAGT-----PVTAPLAGNI 533

QY 65 SKILVKEGDTVKGQTVLVLEAMKMETEINAPTDGKVEKVLVKERDAVQGGQGLIKI 121
Db 534 WKVIATEGQSVAEAGDVLVLEAMKMETEIRAAQAAGTVRGIAVKSQDAVSVGDTLMTL 590

RESULT 21
F64453
oxaloacetate decarboxylase (EC 4.1.1.3) alpha chain MJ1231 [similarity] - Methanococcus
C:Species: Methanococcus jannaschii
C>Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 18-Aug-2000
C:Accession: F64453
R;Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake,
; Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.
rson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
Science 273, 1058-1073, 1996
A:Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese,
A:Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschi
A:Reference number: A64300; MUID:96337999; PMID:8688087
A:Accession: F64453
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-567 <BUL>
A:Cross-references: GB:U67563; GB:L77117; NID:G2826379; PIDN:AAB99233.1; PID:G1591862;
C:Genetics:
A:Map position: REV1175190-1173487
C:Superfamily: Klebsiella pneumoniae oxaloacetate decarboxylase alpha chain; lipoyl/bio
C:Keywords: carbon-carbon lyase; carboxy-lyase
F;494-567/Domain: lipoyl/biotin-binding homology <LPB>
F;533/Binding site: biotin (Lys) (covalent) #status predicted

Query Match 28.1%; Score 173; DB 2; Length 567;
```


C;Superfamily: propionyl-CoA carboxylase alpha chain; biotin carboxylase homology; lipoyl F;527-600/Domain: lipoyl/biotin-binding homology <LPB>

Query Match 27.0%; Score 166; DB 2; Length 600;
Best Local Similarity 35.7%; Pred. No. 7.7e-06;
Matches 45; Conservative 18; Mismatches 51; Indels 12; Gaps 3;

QY 2 KLKVTVNGTAYDVDVDKSHEN-----PMGTILFGGTTGGAPAPAAAGGAGAGKAGEGE- 55
Db KVVVEIDGRREVEVSLPADLALNSGGGCDPVGVI-----RRKPKPRKRGHAHTGAAASGDA 533
QY 56 IPAPLAGTYSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTQKVEKVLVKERDAVQGG 115
Db VTAPMQGTIVVKEFAVEEGQEVVAGDLVVLEAMKMNENPVTAHKDGTITGLAVEAGAAITQG 593
QY 116 QGLIKI 121
Db TVLAEI 599

RESULT 26
A83978
pyruvate carboxylase pycA [imported] - Bacillus halodurans (strain C-125)
C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
C;Accession: A83978
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hira
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: A83978
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1150 <STO>
A;Cross-references: GB:AP001516; GB:BA000004; NID:g10175192; PIDN:BAB06344.1; GSPDB:GN00
A;Experimental source: strain C-125
C;Genetics:
A;Gene: pycA
C;Superfamily: pyruvate carboxylase; biotin carboxylase homology; lipoyl/biotin-binding

Query Match 26.8%; Score 165; DB 2; Length 1150;
Best Local Similarity 47.3%; Pred. No. 1.8e-05;
Matches 35; Conservative 14; Mismatches 25; Indels 0; Gaps 0;

QY 48 AGKAGEGEIPAPLAGTYSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTQKVEKVLVK 107
Db 1074 ADKSNPNHIGASMPGTVVKALVEKDKVKQGDHLMITEAMKMETTVQAPDGEVVALHVK 1133
QY 108 ERDAVQGGGLIKI 121
Db DGDALQTGDLLEIV 1147

RESULT 27
G87517
acetyl/propionyl-CoA carboxylase, alpha subunit [imported] - Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 10-May-2001
C;Accession: G87517
R;Niernman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Accession: G87517
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-654 <STO>
A;Cross-references: GB:AE005673; NID:g13423663; PIDN:AAK24139.1; GSPDB:GN00148
C;Genetics:
A;Gene: CC2168
C;Superfamily: propionyl-CoA carboxylase alpha chain; biotin carboxylase homology; lipoyl

Query Match 26.7%; Score 164; DB 2; Length 654;
Best Local Similarity 31.0%; Pred. No. 1.2e-05;
Matches 48; Conservative 12; Mismatches 39; Indels 56; Gaps 4;

QY 1 MKLKVTVNGTAYDVDVDKSHENPMGTILFGGTT----- 35
Db MHLPMSTDGKA-----TPLRVALIGGGTSDWDIRHADGSTFDEVTRLPITY 549
QY 36 GGAP-----APAAAGGAGAGKAGEGEIPAPLAGTYSKILVKEGDTVKAGQTV 81
Db GRGPIQVFEGGDVQEFDFVAKIGGAGEGGASDGAILLSPEMGKIVSVSAGQTVSKGQTL 609
QY 82 LVLEAMKMETEINAPTQKVEKVLVKERDAVQGGQ 116
Db LTLEAMKMEHAMAAPFDG-----VVAELSAVAGGQ 639

RESULT 28
D69510
oxaloacetate decarboxylase, biotin carboxyl carrier subunit homolog - Archaeoglobus fu
C;Species: Archaeoglobus fulgidus
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 20-Aug-1999
C;Accession: D69510
R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodsc
.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.E
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S
Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archae
A;Reference number: A69250; MUID:98049343; PMID:9389475
A;Accession: D69510
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-142 <KLE>
A;Cross-references: GB:AE000960; GB:AE000782; NID:g2689283; PIDN:AAB89171.1; PID:g26484
C;Superfamily: biotin carboxyl carrier protein; lipoyl/biotin-binding homology
F;66-139/Domain: lipoyl/biotin-binding homology <LPB>

Query Match 26.5%; Score 163; DB 2; Length 142;
Best Local Similarity 50.8%; Pred. No. 3.1e-06;
Matches 33; Conservative 13; Mismatches 19; Indels 0; Gaps 0;

QY 51 AGEGEIPAPLAGTYSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTQKVEKVLVKERD 110
Db APENAVTSMPLPGVWLKILVKGPKVKGEPWVIVSMKMEINEIVSPTGVAEILVKEGQ 127
QY 111 AVQGG 115
Db 128 RIEAG 132

RESULT 29
G86999
hypothetical protein bcca [imported] - Mycobacterium leprae
C;Species: Mycobacterium leprae
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 10-May-2001
C;Accession: G86999
R;Cole, S.T.; Eiglmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; I
R.; Davies, R.M.; Devlin, K.; Duthoy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holroyd
eam, M.A.; Rutherford, K.M.
Nature 409, 1007-1011, 2001
A;Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; S
A;Title: Massive gene decay in the leprosy bacillus.
A;Reference number: A86909; MUID:21128732; PMID:11234002
A;Accession: G86999
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-598 <STO>
A;Cross-references: GB:AL450380; NID:g13092853; PIDN:CAC30235.1; GSPDB:GN00147
C;Genetics:
A;Gene: bcca

Wed Mar 3 11:42:54 2004 us-09-987-485a-1.rpr

C;Superfamily: propionyl-CoA carboxylase alpha chain; biotin carboxylase homology; lipoy

Query Match 26.5%; Score 163; DB 2; Length 598;
Best Local Similarity 37.3%; Pred. No. 1.3e-05;
Matches 44; Conservative 15; Mismatches 57; Indels 2; Gaps 2;

QY 5 VTVNGTAYDVVDVVDKSHENPMGTILFGGGTGGAPAPAAAGGAGAGKAGEGE-IPAPLAGT 63
Db 481 VEVDGRRLEVSPLADLANPAGCNP-AGVIRKKPKPRKRGHTGAATSGDAVTAPMQGT 539

QY 64 VSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVLVKERDAVQGGGLIKI 121
Db 540 VVKVAEAGQVTMTGDLVVVLEAMKMENPVTAKHKGIIITGLAVEAGTAITQGTVLAEI 597

RESULT 30
A55579
biotin carboxyl carrier protein - Mycobacterium leprae
C;Species: Mycobacterium leprae
C;Date: 25-Aug-1995 #sequence_revision 25-Aug-1995 #text_change 11-Jan-2002
C;Accession: A55579; S22188
R;Norman, E.; De Smet, K.A.L.; Stoker, N.G.; Ratledge, C.; Wheeler, P.R.; Dale, J.W.
J. Bacteriol. 176, 2525-2531, 1994
A;Title: Lipid synthesis in mycobacteria: characterization of the biotin carboxyl carrier
A;Reference number: A55579; MUID:94222829; PMID:7909542
A;Accession: A55579
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-598 <NOR>
A;Cross-references: EMBL:X63470; NID:g44395; PIDN:CAA45070.1; PID:g581342
C;Genetics:
A;Start codon: GTG
C;Superfamily: propionyl-CoA carboxylase alpha chain; biotin carboxylase homology; lipoy
C;Keywords: biotin binding
F;11-463/Domain: biotin carboxylase homology <BCH>
F;525-598/Domain: lipoyl/biotin-binding homology <LPB>
F;564/Binding site: biotin (Lys) (covalent) #status predicted

Query Match 26.5%; Score 163; DB 2; Length 598;
Best Local Similarity 37.3%; Pred. No. 1.3e-05;
Matches 44; Conservative 15; Mismatches 57; Indels 2; Gaps 2;

QY 5 VTVNGTAYDVVDVVDKSHENPMGTILFGGGTGGAPAPAAAGGAGAGKAGEGE-IPAPLAGT 63
Db 481 VEVDGRRLEVSPLADLANPAGCNP-AGVIRKKPKPRKRGHTGAATSGDAVTAPMQGT 539

QY 64 VSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVLVKERDAVQGGGLIKI 121
Db 540 VVKVAEAGQVTMTGDLVVVLEAMKMENPVTAKHKGIIITGLAVEAGTAITQGTVLAEI 597

RESULT 31
S71009
biotin carboxylase protein A2 - Saccharopolyspora erythraea
C;Species: Saccharopolyspora erythraea
C;Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 20-Jun-2000
C;Accession: S71009
R;Donadio, S.; Staver, M.J.; Katz, L.
Mol. Microbiol. 19, 977-984, 1996
A;Title: Erythromycin production in Saccharopolyspora erythraea does not require a function
A;Reference number: S71005; MUID:96249691; PMID:8830278
A;Accession: S71009
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-591 <DON>
A;Cross-references: EMBL:X92557; NID:g1177651; PIDN:CAA63311.1; PID:g1177653
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1995
C;Genetics:
A;Gene: bcpA2
A;Start codon: GTG
C;Superfamily: propionyl-CoA carboxylase alpha chain; biotin carboxylase homology; lipoy
F;12-463/Domain: biotin carboxylase homology <BCH>
F;517-590/Domain: lipoyl/biotin-binding homology <LPB>

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Query Match 26.3%; Score 162; DB 2; Length 591;
Best Local Similarity 35.9%; Pred. No. 1.6e-05;
Matches 42; Conservative 18; Mismatches 51; Indels 6; Gaps 3;

QY 5 VTVNGTAYDVVDVVDKSHENPMGTILFGGGTGGAPAPAAAGGAGAGKAGEGEIPAPLAGTV 64
Db 479 VEVGRRLEVSPLADLT---PAAAP--AGGAGRRRRRSAGGGAGSSGDA-VTAPMQGTL 532

QY 65 SKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVLVKERDAVQGGGLIKI 121
Db 533 VKLVVAEGDRVSAGDEIAVLEAMKMENPVLAKHKGTVTGLTAQPGATLTQGSTLCEL 589

RESULT 32
S71006
biotin carboxylase protein A1 - Saccharopolyspora erythraea
C;Species: Saccharopolyspora erythraea
C;Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 20-Jun-2000
C;Accession: S71006
R;Donadio, S.; Staver, M.J.; Katz, L.
Mol. Microbiol. 19, 977-984, 1996
A;Title: Erythromycin production in Saccharopolyspora erythraea does not require a function
A;Reference number: S71005; MUID:96249691; PMID:8830278
A;Accession: S71006
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-597 <DON>
A;Cross-references: EMBL:X92556; NID:g1177647; PIDN:CAA63308.1; PID:g1177649
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1995
C;Genetics:
A;Gene: bcpA1
A;Start codon: GTG
C;Superfamily: propionyl-CoA carboxylase alpha chain; biotin carboxylase homology; lipoy
F;18-469/Domain: biotin carboxylase homology <BCH>
F;523-596/Domain: lipoyl/biotin-binding homology <LPB>

Query Match 26.3%; Score 162; DB 2; Length 597;
Best Local Similarity 35.9%; Pred. No. 1.6e-05;
Matches 42; Conservative 18; Mismatches 51; Indels 6; Gaps 3;

QY 5 VTVNGTAYDVVDVVDKSHENPMGTILFGGGTGGAPAPAAAGGAGAGKAGEGEIPAPLAGTV 64
Db 485 VEVGRRLEVSPLADLT---PAAAP--AGGAGRRRRRSAGGGAGSSGDA-VTAPMQGTL 538

QY 65 SKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVLVKERDAVQGGGLIKI 121
Db 539 VKLVVAEGDRVSAGDEIAVLEAMKMENPVLAKHKGTVTGLTAQPGATLTQGSTLCEL 595

RESULT 33
AE2911
pyruvate carboxylase [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
C;Accession: AE2911
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, J.; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, ster, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; MUID:21608550; PMID:11743193
A;Accession: AE2911
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1174 <XUR>
A;Cross-references: GB:AE008688; PIDN:AAL43707.1; PID:g17741236; GSPDB:GN00186
A;Experimental source: strain C58 (Dupont)
C;Genetics:
A;Gene: pycA
A;Map position: circular chromosome

C;Superfamily: pyruvate carboxylase; biotin carboxylase homology; lipoyl/biotin-binding

Query Match 26.3%; Score 161.5; DB 2; Length 1174;
Best Local Similarity 36.2%; Pred. No. 3.4e-05;
Matches 47; Conservative 17; Mismatches 45; Indels 21; Gaps 5;

QY 2 KLKVTVNGTAYDVDVDKSHENPMGTILFGGGTGGA-----PAAGGAGAGKAG 52
Db 1050 KTLVIVNQASSGID---DKG---MVTVFF--EINGQPRRIKVPDRAHGASGSAVRKAE 1100

QY 53 EG---EIPAPLAGTVSKILVKEGDTVKGQTVLVLEAMKMETEINAPTQKVKVVKER 109
Db 1101 PGNASHIGAPMPGVISRVFINQGEVKAGDVLISIEAMKMETALHAERDGGKIAEVLVKPG 1160

QY 110 DAVQGGQGLI 119
Db 1161 DQIDAKDLLI 1170

RESULT 34

C97686 pyruvate carboxylase (U51439) [imported] - Agrobacterium tumefaciens (strain C58, Cereon

C;Species: Agrobacterium tumefaciens
C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 18-Nov-2002

C;Accession: C97686
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Quorollo, B.; Goldman,

A.; Liu, F.; Wollam, C.; Allinger, M.; Dougherty, D.; Scott, C.; Lappas, C.; Markelz, B.;
Science 294, 2323-2328, 2001

A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
A;Reference number: A97359; MUID:21608551; PMID:11743194

A;Accession: C97686
A;Status: preliminary
A;Molecule type: DNA

A;Residues: 1-1174 <KUR>
A;Cross-references: GB:AE007869; PIDN:AAK88444.1; PID:gl5157941; GSPDB:GN00169

C;Genetics:
A;Gene: AGR_C_4940

A;Map position: circular chromosome
C;Superfamily: pyruvate carboxylase; biotin carboxylase homology; lipoyl/biotin-binding

Query Match 26.3%; Score 161.5; DB 2; Length 1174;
Best Local Similarity 36.2%; Pred. No. 3.4e-05;
Matches 47; Conservative 17; Mismatches 45; Indels 21; Gaps 5;

QY 2 KLKVTVNGTAYDVDVDKSHENPMGTILFGGGTGGA-----PAAGGAGAGKAG 52
Db 1050 KTLVIVNQASSGID---DKG---MVTVFF--EINGQPRRIKVPDRAHGASGSAVRKAE 1100

QY 53 EG---EIPAPLAGTVSKILVKEGDTVKGQTVLVLEAMKMETEINAPTQKVKVVKER 109
Db 1101 PGNASHIGAPMPGVISRVFINQGEVKAGDVLISIEAMKMETALHAERDGGKIAEVLVKPG 1160

QY 110 DAVQGGQGLI 119
Db 1161 DQIDAKDLLI 1170

RESULT 35

G97819 hypothetical protein pcca [imported] - Rickettsia conorii (strain Malish 7)

C;Species: Rickettsia conorii
C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 22-Oct-2001

C;Accession: G97819
R;Ogata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, D.; R

Science 293, 2093-2098, 2001
A;Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii.

A;Reference number: A97700; MUID:21442074; PMID:11557893
A;Accession: G97819

A;Status: preliminary
A;Molecule type: DNA

A;Residues: 1-665 <KUR>
A;Cross-references: GB:AE006914; PIDN:AAL03497.1; PID:gl5620071; GSPDB:GN00173

C;Genetics:
A;Molecule type: DNA

A;Gene: pcca
C;Superfamily: propionyl-CoA carboxylase alpha chain; biotin carboxylase homology; lip

Query Match 25.9%; Score 159; DB 2; Length 665;
Best Local Similarity 50.0%; Pred. No. 3.1e-05;
Matches 33; Conservative 12; Mismatches 21; Indels 0; Gaps 0;

QY 55 EIPAPLAGTVSKILVKEGDTVKGQTVLVLEAMKMETEINAPTQKVKVVKERDAVQG 114
Db 598 ELQAPLSGQIAAIKVKEGQEVTAQGEIMILTAMKMNILAEKIDGKIATFVNEKDNVIR 657

QY 115 GQGLIK 120
Db 658 GQVLE 663

RESULT 36

B71373 probable oxaloacetate decarboxylase, subunit alpha (oadA) - syphilis spirochete

C;Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
C;Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 18-Aug-2000

C;Accession: B71373
R;Fraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gw

rson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; MCI
they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.

Science 281, 375-388, 1998
A;Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.

A;Reference number: A71250; MUID:98332770; PMID:9665876
A;Accession: B71373

A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA

A;Residues: 1-593 <COL>
A;Cross-references: GB:AE001190; GB:AE000520; NID:g3322303; PIDN:AAC65051.1; PID:g3322

A;Experimental source: strain Nichols
C;Genetics:
A;Gene: TP0056

C;Superfamily: Klebsiella pneumoniae oxaloacetate decarboxylase alpha chain; lipoyl/bi
F:510-593/Domain: lipoyl/biotin-binding homology <LPB>
F:560/Binding site: biotin (Lys) (covalent) #status predicted

Query Match 25.8%; Score 158.5; DB 2; Length 593;
Best Local Similarity 35.4%; Pred. No. 3e-05;
Matches 45; Conservative 18; Mismatches 43; Indels 21; Gaps 3;

QY 6 TVNGTAYDVDVDKSHENPMGTILFGGGTGGA-----PAAGGAGAGKAGAGEI----- 56
Db 476 TVNGTAYTVVQE-----GAVLRVNGTPYTVRVEAGPSVAGTSGGTVTAKVGACT 526

QY 57 --PAPLAGTVSKILVKEGDTVKGQTVLVLEAMKMETEINAPTQKVKVVKERDAVQG 114
Db 527 TLPAPVAGSVVKHTVQDGTATVNSGETVLMVESMKMELEVKATAAGTIH-FLIAPGAHVSA 585

QY 115 GQGLIKI 121
Db 586 GQVLAEI 592

RESULT 37

A95049 hypothetical protein SP0423 [imported] - Streptococcus pneumoniae (strain TIGR4)

C;Species: Streptococcus pneumoniae
C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 24-Aug-2001

C;Accession: A95049
R;Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; He

on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple,
nson, T.; Hickey, E.K.; Holt, I.E.

Science 293, 498-506, 2001
A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morris

A;Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
A;Reference number: A95000; MUID:21357209; PMID:11463916

A;Accession: A95049
A;Status: preliminary
A;Molecule type: DNA

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OM protein - protein search, using sw model

Run on: March 3, 2004, 10:24:54 ; Search time 12.7083 Seconds
(without alignments)
499.873 Million cell updates/sec

Title: US-09-987-485A-1
Perfect score: 615
Sequence: 1 MKLKVTVNGTAYDVEDVDK.....KVLVKERDAVGGQGLIKIG 122

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	604.5	98.3	123	1 BCCP_PROFR	P02904 propionibac
2	200.5	32.6	595	1 DCOA_KLEPN	P13187 klebsiella
3	175.5	28.5	590	1 DCOA_SALTY	Q03030 salmonella
4	173	28.1	567	1 PYCB_METJA	Q58628 methanococc
5	168	27.3	130	1 BCCP_STRMU	P29337 streptococc
6	163	26.5	598	1 BCCA_MYCLE	P46392 mycobacteri
7	159	25.9	717	1 MCCA_MOUSE	Q99mr8 mus musculu
8	153	24.9	725	1 MCCA_HUMAN	Q96rq3 homo sapien
9	143	23.3	70	1 BCCP_LYCES	P05115 lycopersico
10	143	23.3	734	1 MCCA_ARATH	Q42523 arabidopsis
11	141	22.9	568	1 PYCB_METTH	O27179 methanobact
12	138.5	22.5	157	1 BCCP_PORPU	P51283 porphyra pu
13	138	22.4	1180	1 PYC2_YEAST	P32327 saccharomyc
14	133.5	21.7	163	1 BCCP_CHLMU	Q9pkr5 chlamydia m
15	133	21.6	1178	1 PYC1_YEAST	P11154 saccharomyc
16	132	21.5	1189	1 PYC_PICPA	P78992 pichia past
17	131	21.3	164	1 BCCP_CHLTR	O84125 chlamydia t
18	130	21.1	629	1 ODP2_ECOLI	P06959 escherichia
19	130	21.1	731	1 MCCA_SOYBN	Q42777 glycine max
20	129.5	21.1	181	1 BCCP_ANASP	Q06881 anabaena sp
21	129	21.0	547	1 ODP2_PSEAE	Q59638 pseudomonas
22	129	21.0	1178	1 PYC_MOUSE	Q05920 mus musculu
23	128	20.8	544	1 ODP2_ACHLA	P35489 acholeplasm
24	125.5	20.4	654	1 BCCA_MYCTU	P46401 mycobacteri
25	123.5	20.1	637	1 ODP2_AZOVI	P10802 azotobacter
26	122	19.8	553	1 ODP2_ALCEU	Q59098 alcaligenes
27	121	19.7	1178	1 PYC_HUMAN	P11498 homo sapien
28	119	19.3	1178	1 PYC_RAT	P52873 rattus norv
29	118.5	19.3	704	1 PCCA_RAT	P14882 rattus norv
30	118	19.2	70	1 BTB7_MYCSM	Q9xcd6 mycobacteri
31	117	19.0	156	1 BCCP_PSEAE	P37799 pseudomonas
32	115	18.7	70	1 BTB7_MYCTU	O05845 mycobacteri
33	115	18.7	262	1 BCCP_SOYBN	Q42783 glycine max

34	114	18.5	438	1 ODP2_MYCCA	Q49110 mycoplasma
35	112	18.2	155	1 BCCP_HAEIN	P43874 haemophilus
36	110	17.9	703	1 PCCA_HUMAN	P05165 homo sapien
37	108.5	17.6	167	1 BCCP_CHLPN	Q92901 chlamydia p
38	108	17.6	553	1 ODO2_MYCTU	Q10381 mycobacteri
39	107	17.4	70	1 BTB7_MYCLE	Q9cch9 mycobacteri
40	105.5	17.2	567	1 ODP2_HAEIN	P45118 haemophilus
41	104	16.9	1835	1 DUR1_YEAST	P32528 saccharomyc
42	103	16.7	462	1 ODPB_ZYMMO	O66113 zymomonas m
43	102.5	16.7	156	1 BCCP_ECOLI	P02905 escherichia
44	97	15.8	384	1 ODP2_MYCGE	P47514 mycoplasma
45	95.5	15.5	463	1 ODO2_YEAST	P19262 saccharomyc

ALIGNMENTS

RESULT 1
BCCP_PROFR
ID BCCP_PROFR STANDARD; PRT; 123 AA.
AC P02904;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Biotin carboxyl carrier protein of methylmalonyl-CoA carboxyl-
transferase (Transcarboxylase, 1.3S subunit).
OS Propionibacterium freudenreichii shermanii.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Propionibacterineae; Propionibacteriaceae; Propionibacterium.
OX NCBI_TaxID=1752;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85298212; PubMed=3898065;
RA Murtif V.L., Bahler C.R., Samols D.;
RT "Cloning and expression of the 1.3S biotin-containing subunit of
transcarboxylase.";
RL Proc. Natl. Acad. Sci. U.S.A. 82:5617-5621(1985).
RN [2]
RP SEQUENCE.
RX MEDLINE=80049796; PubMed=40985;
RA Maloy W.L., Bowien B.U., Zwolinski G.K., Kumar G.K., Wood H.G.,
RA Ericsson L.H., Walsh K.A.;
RT "Amino acid sequence of the biotinyl subunit from transcarboxylase.";
RL J. Biol. Chem. 254:11615-11622(1979).
RN [3]
RP MUTAGENESIS OF ALA-87; MET-88; LYS-89 AND MET-90.
RX MEDLINE=92406744; PubMed=1526981;
RA Shenoy B.C., Xie Y., Park V.L., Kumar G.K., Beegen H., Wood H.G.,
RA Samols D.;
RT "The importance of methionine residues for the catalysis of the
biotin enzyme, transcarboxylase. Analysis by site-directed
mutagenesis.";
RL J. Biol. Chem. 267:18407-18412(1992).
RN [4]
RP STRUCTURE BY NMR.
RX MEDLINE=98066416; PubMed=9398186;
RA Reddy D.V., Shenoy B.C., Carey P.R., Soennichsen F.D.;
RT "Absence of observable biotin-protein interactions in the 1.3S
subunit of transcarboxylase: an NMR study.";
RL Biochemistry 36:14676-14682(1997).
CC -1- FUNCTION: THE BIOTINYL 1.3S SUBUNIT SERVES AS A CARBOXYL CARRIER
BETWEEN THE SUBSTRATE BINDING SITES ON THE 12S AND 5S SUBUNITS.
CC -1- SUBUNIT: TRANSCARBOXYLASE IS COMPOSED OF THREE SUBUNITS: 1.3S,
5S, AND 12S. THE CORE OF THE ENZYME IS COMPOSED OF SIX 12S
SUBUNITS. ON EACH SIDE OF THE CORE THERE ARE THREE PAIRS OF 5S
SUBUNITS. EACH 5S DIMER IS ATTACHED TO THE CORE BY TWO 1.3S
SUBUNITS. THUS THE TOTAL NUMBER OF CHAINS IS 30 (6 + 12 + 12).

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DR EMBL; AE008854; AAL22221.1; -.
DR PIR; B44465; B44465.
DR HSSP; P02905; 1A6X.
DR StyGene; SG10259; oadA1.
DR StyGene; SG????; oadA2.
DR InterPro; IPR001882; Biotin_BS.
DR InterPro; IPR000089; Biotin_lipoyl.
DR InterPro; IPR000891; HMGL-like.
DR InterPro; IPR005776; Oada.
DR InterPro; IPR003379; PYC_OADA.
DR Pfam; PF00364; biotin_lipoyl; 1.
DR Pfam; PF00682; HMGL-like; 1.
DR Pfam; PF02436; PYC_OADA; 1.
DR TIGRFAMS; TIGR01108; oada; 1.
DR PROSITE; PS00188; BIOTIN; 1.
KW Decarboxylase; Lyase; Sodium transport; Biotin; Complete proteome.
FT INIT MET 0
FT BINDING 556 556 BIOTIN (BY SIMILARITY).
FT SEQUENCE 590 AA; 63075 MW; 4EA421F9324AFD7B CRC64;
Query Match 28.5%; Score 175.5; DB 1; Length 590;
Best Local Similarity 37.5%; Pred. No. 3.2e-06;
Matches 48; Conservative 10; Mismatches 41; Indels 29; Gaps 3;
QY 5 VTVNGTAYDVDDVKSHENPMGTILFGGG-----TGGAPAPAAAGGAGAGKAGE 53
Db 480 VEVEGKAFVVKVS-----DGGDISQLTAAVPAASSAPVQAAAPAGAGT--- 522
QY 54 GEIPAPLAGTVSKILVKEGDTVKGQTVLVLEAMKMETEINAPTDGKVEKVLVKERDAVQ 113
Db 523 -PVTAPLAGNIWKVIATEGQTVAEQGVLLILEAMKMETEIRAAQAGTVRGIAVKSGDAVS 581
QY 114 GGQGLIKI 121
Db 582 VGDTLMTL 589
RESULT 4
PYCB_METJA STANDARD; PRT; 567 AA.
AC Q58628;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Pyruvate carboxylase subunit B (EC 6.4.1.1) (Pyruvic carboxylase B).
GN PYCB OR MJ1231.
OS Methanococcus jannaschii.
OC Archaea; Euryarchaeota; Methanococci; Methanococcales;
OC Methanocaldococcaceae; Methanocaldococcus.
OX NCBI_TaxID=2190;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
RX MEDLINE=96337999; PubMed=8688087;
RA Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,
RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
RA Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
RA Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
RA Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
RT "Complete genome sequence of the methanogenic archaeon, Methanococcus
RT jannaschii."
RL Science 273:1058-1073(1996).
RN [2]
RP SEQUENCE OF 190-125; 260-270; 277-289; 277-289; 309-325; 328-358;
RP 370-380; 386-409; 422-438; 491-506 AND 491-506, AND FUNCTION.
RX MEDLINE=21034791; PubMed=11195096;
RA Mukhopadhyay B., Patel V.J., Wolfe R.S.;
RT "A stable archaeal pyruvate carboxylase from the hyperthermophile
RT Methanococcus jannaschii."
RL Arch. Microbiol. 174:406-414(2000).
```

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CC -!- FUNCTION: Pyruvate carboxylase catalyzes a 2-step reaction,
CC involving the ATP-dependent carboxylation of the covalently
CC attached biotin in the first step and the transfer of the carboxyl
CC group to pyruvate in the second.
CC -!- CATALYTIC ACTIVITY: ATP + pyruvate + HCO(3)(-) = ADP + phosphate +
CC oxaloacetate.
CC -!- COFACTOR: ATP, magnesium (or manganese or cobalt), pyruvate and
CC bicarbonate.
CC -!- ENZYME REGULATION: INHIBITED BY MAGNESIUM, WHEN ITS CONCENTRATION
CC EXCEEDED THE ATP ONE, AND BY HIGH CONCENTRATION OF ATP AND ALPHA-
CC KETOGLUTARATE.
CC -!- PATHWAY: Gluconeogenesis.
CC -!- SUBUNIT: Heterooctamer of four A and four B subunits.
CC -!- MASS SPECTROMETRY: MW=64160; METHOD=MALDI.
CC -!- MISCELLANEOUS: ITS OPTIMUM PH IS 8.5 AND THE OPTIMUM TEMPERATURE
CC IS 80-90 DEGREES CELSIUS.
CC -!- SIMILARITY: WITH OTHER BIOTIN CARBOXYLASES, LIPOAMIDE TRANSFERASES
CC AND CARBAMYL PHOSPHATE SYNTHETASES.
CC -----
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CC -----
CC EMBL; U67563; AAB99233.1; -.
CC PIR; F64453; F64453.
CC HSSP; P02905; 1A6X.
CC TIGR; MJ1231; -.
CC InterPro; IPR001882; Biotin_BS.
CC InterPro; IPR000089; Biotin_lipoyl.
CC InterPro; IPR000891; HMGL-like.
CC InterPro; IPR005776; Oada.
CC InterPro; IPR003379; PYC_OADA.
CC Pfam; PF00364; biotin_lipoyl; 1.
CC Pfam; PF00682; HMGL-like; 1.
CC Pfam; PF02436; PYC_OADA; 1.
CC TIGRFAMS; TIGR01108; oada; 1.
CC PROSITE; PS00188; BIOTIN; 1.
KW Ligase; Multifunctional enzyme; Gluconeogenesis; Magnesium; Pyruvate;
KW Biotin; Complete proteome.
FT BINDING 52 60 PYRUVATE (BY SIMILARITY).
FT BINDING 533 533 BIOTIN (BY SIMILARITY).
SQ SEQUENCE 567 AA; 63907 MW; 5E07800622545628 CRC64;
Query Match 28.1%; Score 173; DB 1; Length 567;
Best Local Similarity 50.7%; Pred. No. 4.8e-06;
Matches 35; Conservative 12; Mismatches 22; Indels 0; Gaps 0;
QY 53 EGEIPAPLAGTVSKILVKEGDTVKGQTVLVLEAMKMETEINAPTDGKVEKVLVKERDAV 112
Db 498 EGAVTSPFRGMVTKIKVKEGDKVKKGDVIVVLEAMKMEHPESPVEGTVERILIDEGDAV 557
QY 113 QGGQGLIKI 121
Db 558 NVGDVIMII 566
RESULT 5
BCCP_STRMU STANDARD; PRT; 130 AA.
AC P29337;
DT 01-DEC-1992 (Rel. 24, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Biotin carboxyl carrier protein (BCCP).
GN BCC OR SMU.1016.
OS Streptococcus mutans.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1309;
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RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=UT-041 / Serotype C;
RX  MEDLINE=9315978; PubMed=8431283;
RA  Wang D., Wayne M.M., Taricani M., Buckingham K., Sandham H.J.;
RT  "Biotin-containing protein as a cause of false positive clones in
RL  gene probing with streptavidin/biotin.";
RN  BioTechniques 14:209-212(1993).
RP  [2]
RC  SEQUENCE FROM N.A.
RX  STRAIN=UA159 / ATCC 700610 / Serotype C;
RA  Ajdic D., McShan W.M., McLaughlin R.E., Savic G., Chang J.,
RT  Carson M.B., Primeaux C., Tian R., Kenton S., Jia H., Lin S., Qian Y.,
RL  Li S., Zhu H., Najjar F., Lai H., White J., Roe B.A., Ferretti J.J.;
RN  "Genome sequence of Streptococcus mutans UA159, a cariogenic dental
RP  pathogen.";
RC  Proc. Natl. Acad. Sci. U.S.A. 99:14434-14439(2002).
CC  -----
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CC  or send an email to license@isb-sib.ch).
CC  -----
CC  EMBL; M80523; AAA03702.1; -.
CC  EMBL; AE014941; AAN58716.1; -.
CC  HSSP; P02905; 1A6X.
CC  InterPro; IPR001882; Biotin_BS.
CC  InterPro; IPR000089; Biotin_lipoyl.
CC  Pfam; PF00364; biotin_lipoyl; 1.
CC  PROSITE; PS00188; BIOTIN; 1.
KW  Fatty acid biosynthesis; Biotin; Complete proteome.
FT  BINDING 96 96 BIOTIN (BY SIMILARITY).
FT  CONFLICT 121 121 N -> D (IN REF. 1).
SQ  SEQUENCE 130 AA; 13600 MW; A0DEA05EC46FF00B CRC64;

Query Match 27.3%; Score 168; DB 1; Length 130;
Best Local Similarity 34.4%; Pred. NO. 2.9e-06;
Matches 45; Conservative 18; Mismatches 52; Indels 16; Gaps 3;

QY 2 KLVTVNGTAYDVVDVVDKSHENPMGTIL--FGGGTGA-----PAPAAGGAGAGK 50
DB 4 KFKISIDGKEYLVEMEEISESSVPAATPTPTTENTRAASDKQSQSTPSAATASAA-- 61

QY 51 AGEGEIPAPLAGTVSKILVKEGDTVAGQTVLVLEAMKMETEINAPTDGKVEKVLVKERD 110
DB 62 ---NTMPAPMPGTILKVLNVGDTVSENQPLMLEAMKMEINEIVAGMAGTVSAIHVSSGQ 118

QY 111 AVQGGQGLIKI 121
DB 119 TVNAGDNLITI 129

RESULT 6
BCCA_MYCLE STANDARD; PRT; 598 AA.
AC P46352;
DT 01-NOV-1995 (Rel. 32, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Acetyl-/propionyl-coenzyme A carboxylase alpha chain [Includes: Biotin
DE carboxylase (EC 6.3.4.14); Biotin carboxyl carrier protein (BCCP)].
GN BCCA OR ML0726 OR B1308_C1_129.
OS Mycobacterium leprae.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1769;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94222829; PubMed=7909542;
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RA Norman E., de Smet K.A.L., Stoker N.G., Ratledge C., Wheeler P.R.,
RA Dale J.W.;
RT "Lipid synthesis in mycobacteria: characterization of the biotin
RT carboxyl carrier protein genes from Mycobacterium leprae and M.
RT tuberculosis.";
RL J. Bacteriol. 176:2525-2531(1994).
RN [2]
RP SEQUENCE FROM N.A.
RA Smith D.R., Robison K.;
RL Submitted (MAR-1994) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=TN;
RX MEDLINE=21128732; PubMed=11234002;
RA Cole S.T., Eiglmeier K., Parkhill J., James K.D., Thomson N.R.,
RA Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D.,
RA Mungall K., Basham D., Brown D., Chillingworth T., Connor R.,
RA Davies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N.,
RA Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S.,
RA Murphy L., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M.,
RA Rutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R.,
RA Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R.,
RA Barrell B.G.;
RT "Massive gene decay in the leprosy bacillus.";
RL Nature 409:1007-1011(2001).
CC -!- FUNCTION: THIS PROTEIN CARRIES TWO FUNCTIONS: BIOTIN CARBOXYL
CC CARRIER PROTEIN AND BIOTIN CARBOXYLTRANSFERASE.
CC -!- CATALYTIC ACTIVITY: ATP + biotin-carboxyl-carrier protein + CO(2)
CC = ADP + phosphate + carboxybiotin-carboxyl-carrier protein.
CC -!- COFACTOR: Biotin.
CC -!- PATHWAY: Long-chain fatty acid biosynthesis; first step.
CC -!- SUBUNIT: MULTIMER COMPRISED OF 2 DIFFERENT SUBUNITS, THE LARGER
CC ONE (63/64 kDa) HAS BIOTIN CARBOXYLASE AND BIOTIN CARRIER
CC FUNCTIONS, WHILE THE SMALLER SUBUNIT POSSESSES CARBOXYLTRANSFERASE
CC AND SUBSTRATE BINDING ACTIVITY.
CC -!- SIMILARITY: TO OTHER BIOTIN-DEPENDENT ENZYMES AND CARBAMOYL-
CC PHOSPHATE SYNTHETASES.
CC -----
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CC -----
CC EMBL; X63470; CAA45070.1; -.
CC EMBL; U00012; AAA85920.1; -.
CC EMBL; AL583919; CAC30235.1; -.
CC PIR; A55579; A55579.
CC PIR; G86999; G86999.
CC HSSP; P24182; 1BNC.
CC Leproma; ML0726; -.
CC InterPro; IPR001882; Biotin_BS.
CC InterPro; IPR005482; Biotin_carb_C.
CC InterPro; IPR000089; Biotin_lipoyl.
CC InterPro; IPR005479; CPase_L_D2.
CC InterPro; IPR005481; CPase_L_N.
CC Pfam; PF02785; Biotin_carb_C; 1.
CC Pfam; PF00364; biotin_lipoyl; 1.
CC Pfam; PF00289; CPsase_L_D2; 1.
CC Pfam; PF02786; CPsase_L_D2; 1.
CC PROSITE; PS00188; BIOTIN; 1.
CC PROSITE; PS00866; CPsase_1; 1.
CC PROSITE; PS00867; CPsase_2; 1.
KW Fatty acid biosynthesis; Ligase; Biotin; Multifunctional enzyme;
KW ATP-binding; Complete proteome.
FT DOMAIN 11 441 BIOTIN CARBOXYLASE.
FT DOMAIN 532 598 BIOTIN CARBOXYL CARRIER PROTEIN.
FT NP_BIND 169 174 ATP (BY SIMILARITY).
FT ACT_SITE 299 299 BY SIMILARITY.
FT BINDING 564 564 BIOTIN (BY SIMILARITY).
FT CONFLICT 30 30 D -> H (IN REF. 1).
```

SQ SEQUENCE 598 AA; 63863 MW; 5F2E291D7C54515D CRC64;

Query Match 26.5%; Score 163; DB 1; Length 598;
Best Local Similarity 37.3%; Pred. No. 2.8e-05;
Matches 44; Conservative 15; Mismatches 57; Indels 2; Gaps 2;

QY 5 VTVNGTAYDVDVVDKSHENPMGTILFGGGTGAPAPAGGAGAGKAGEGE-IPAPLAGT 63
Db VEVDGRRLEVSPLADLANPAGCNP-AGVIRKKPKRKRGGHTGAATSGDAVTAPMQGT 539

QY 64 VSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVLVKERDAVQGGQGLIKI 121
Db VVKVAEAGQTVMTGDLVVVLEAMKMPVTAHXDGIITGLAVEAGTAITQGTVLAEI 597

RESULT 7

MCCA_MOUSE STANDARD; PRT; 717 AA.

AC Q99MR8; Q9D8R2;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Methylcrotonyl-CoA carboxylase alpha chain, mitochondrial precursor
(EC 6.4.1.4) (3-Methylcrotonyl-CoA carboxylase 1) (MCCase alpha
subunit) (3-methylcrotonyl-CoA:carbon dioxide ligase alpha subunit).
GN MCCC1 OR MCCA.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]

RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=21102410; PubMed=11181649;
RA Baumgartner M.R., Almashanu S., Suormala T., Obie C., Cole R.N.,
RA Packman S., Baumgartner E.R., Valle D.;
RT "The molecular basis of human 3-methylcrotonyl-CoA carboxylase
deficiency.";
RL J. Clin. Invest. 107:495-504 (2001).
RN [2]

RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Pancreas;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King C., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]

RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
CC -!- CATALYTIC ACTIVITY: ATP + 3-methylcrotonyl-CoA + HCO(3) (-) = ADP +
CC phosphate + 3-methylglutaconyl-CoA.
CC -!- COFACTOR: Biotin.
CC -!- PATHWAY: Leucine catabolism.
CC -!- SUBUNIT: Probably a dodecamer composed of six biotin-containing
CC alpha subunits and six beta subunits.
CC -!- SUBCELLULAR LOCATION: Mitochondrial matrix (By similarity).
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF310338; AAC50244.1; -;
DR EMBL; AK007782; BAB25253.1; -;
DR EMBL; BC021382; AAH21382.1; -;
DR HSSP; P24182; 1DVI.
DR MCD; MGI:1919289; Mcccl.
DR GO; GO:0005759; C:mitochondrial matrix; ISS.
DR GO; GO:0009374; F:biotin binding; ISS.
DR GO; GO:0004485; F:methylcrotonyl-CoA carboxylase activity; ISS.
DR GO; GO:0006768; P:biotin metabolism; ISS.
DR GO; GO:0006552; P:leucine catabolism; ISS.
DR InterPro; IPR001882; Biotin_BS.
DR InterPro; IPR005482; Biotin_carb_C.
DR InterPro; IPR000089; Biotin_lipoyl.
DR InterPro; IPR005479; CPase_L_D2.
DR InterPro; IPR005481; CPase_L_N.
DR Pfam; PF02785; Biotin_carb_C; 1.
DR Pfam; PF00364; biotin_lipoyl; 1.
DR Pfam; PF00289; CPase_L_chain; 1.
DR Pfam; PF02786; CPase_L_D2; 1.
DR PROSITE; PS00188; BIOTIN; 1.
DR PROSITE; PS00867; CPASE 2; 1.
KW Mitochondrion; Ligase; Biotin; ATP-binding; Transit peptide.
FT TRANSIT 1 44 MITOCHONDRION (POTENTIAL).
FT CHAIN 45 717 METHYLCROTONYL-COA CARBOXYLASE ALPHA
FT NP_BIND 205 210 ATP (POTENTIAL).
FT ACT_SITE 335 335 BY SIMILARITY.
FT BINDING 677 677 BIOTIN (BY SIMILARITY).
FT DOMAIN 709 714 POLY-GLU.
FT CONFLICT 324 324 R -> K (IN REF. 3).
FT CONFLICT 507 507 A -> P (IN REF. 1).
SQ SEQUENCE 717 AA; 79343 MW; F653FE7AC1E5AA90 CRC64;

Query Match 25.9%; Score 159; DB 1; Length 717;
Best Local Similarity 36.0%; Pred. No. 6.6e-05;
Matches 40; Conservative 17; Mismatches 42; Indels 12; Gaps 3;

QY 3 LKVTNGTAYDVDVDKSH-----ENPMGTILFGGGTG-GAPAPAGGAGAGKAGEGEIP 57
Db LKSSINGVA-----RKSKFILLDNTVHLFSMEGSIEVGIPVPKYLSPVSAEGAQGGTI 646

QY 58 APLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVLVKE 108

Db 647 APMTGTIEKVFVKAGDRVKAGDSLVMVMIAMKMEHTIKAPKDGRIKKVFFSE 697

RESULT 8

MCCA_HUMAN

ID MCCA_HUMAN STANDARD; PRT; 725 AA.

AC Q96RQ3; Q9H959; Q9NS97;

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Methylcrotonyl-CoA carboxylase alpha chain, mitochondrial precursor

DE (EC 6.4.1.4) (3-Methylcrotonyl-CoA carboxylase 1) (MCCase alpha

DE subunit) (3-methylcrotonyl-CoA:carbon dioxide ligase alpha subunit).

GN MCCC1 OR MCCA.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A., AND VARIANTS MCGI ARG-325 AND SER-385.

RX PubMed=11170888;

RA Gallardo M.E., Desviat L.R., Rodriguez J.M., Esparza-Gordillo J.,

RA Perez-Cerda C., Perez B., Rodriguez-Pombo P., Criado O., Sanz R.,

RA Morton D.H., Gibson K.M., Le T.F., Ribes A., Rodriguez de Cordoba S.,

RA Ugarte M., Penalva M.A.;

RT "The molecular basis of 3-methylcrotonylglycinuria, a disorder of

RT leucine catabolism.";

RL Am. J. Hum. Genet. 68:334-346(2001).

RN [2]

RP SEQUENCE FROM N.A., AND VARIANT HIS-464.

RX MEDLINE=21295033; PubMed=11401427;

RA Obata K., Fukuda T., Morishita R., Abe S., Asakawa S., Yamaguchi S.,

RA Yoshino M., Ihara K., Murayama K., Shigemoto K., Shimizu N., Kondo I.;

RT "Human biotin-containing subunit of 3-methylcrotonyl-CoA carboxylase

RT gene (MCCA): cDNA sequence, genomic organization, localization to

RT chromosomal band 3q27, and expression.";

RL Genomics 72:145-152(2001).

RN [3]

RP SEQUENCE FROM N.A., AND VARIANT MCGI PHE-535.

RX MEDLINE=21299419; PubMed=11406611;

RA Holzinger A., Roeschinger W., Lagler F., Mayerhofer P.U., Lichtner P.,

RA Kattenfeld T., Thuy L.P., Nyhan W.L., Koch H.G., Muntau A.C.,

RA Roscher A.A.;

RT "Cloning of the human MCCA and MCCB genes and mutations therein reveal

RT the molecular cause of 3-methylcrotonyl-CoA: carboxylase

RT deficiency.";

RL Hum. Mol. Genet. 10:1299-1306(2001).

RN [4]

RP SEQUENCE FROM N.A., AND VARIANTS MCGI VAL-289; SER-385; PRO-437 AND

RP HIS-532.

RX PubMed=11181649;

RA Baumgartner M.R., Almashanu S., Suormala T., Obie C., Cole R.N.,

RA Packman S., Baumgartner E.R., Valle D.;

RT "The molecular basis of human 3-methylcrotonyl-CoA carboxylase

RT deficiency.";

RL J. Clin. Invest. 107:495-504(2001).

RN [5]

RP SEQUENCE FROM N.A.

RA Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,

RA Nishikawa T., Nagai K., Sugano S., Aotsuka S., Yoshikawa Y.,

RA Matsunawa H., Ishii S., Kawai Y., Saito K., Yamamoto J., Wakamatsu A.,

RA Nakamura Y., Nagahara K., Masuho Y., Sasaki N.;

RT "NEDO human cDNA sequencing project.";

RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.

RN [6]

RP SEQUENCE FROM N.A.

RC TISSUE=Skeletal muscle;

RX MEDLINE=22388257; PubMed=12477932;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner K.H., Sherman C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length

RT human and mouse cDNA sequences.";

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

CC -!- CATALYTIC ACTIVITY: ATP + 3-methylcrotonyl-CoA + HCO(3) (-) = ADP +

CC phosphate + 3-methylglutaconyl-CoA.

CC -!- Cofactor: Biotin.

CC -!- Pathway: Leucine catabolism.

CC -!- SUBUNIT: Probably a dodecamer composed of six biotin-containing

CC alpha subunits and six beta subunits.

CC -!- SUBCELLULAR LOCATION: Mitochondrial matrix.

CC -!- DISEASE: Defects in MCCC1 are the cause of 3-

CC methylcrotonylglycinuria type I (MCGI) [MIM:210200]; also

CC designated CGA or CG2. MCGI is a recessive disease that is

CC characterized by muscular hypotonia and atrophy, probably of

CC spinal origin.

CC -----

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CC -----

DR EMBL; AF310972; AAG53095.1; -.

DR EMBL; AB029826; BAA99407.1; -.

DR EMBL; AF297332; AAK67986.1; -.

DR EMBL; AF310339; AAG50245.1; -.

DR EMBL; AK023051; BAB14377.1; -.

DR EMBL; BC004214; AAH04214.1; -.

DR EMBL; BC004187; AAH04187.1; -.

DR Genew; HGNC:6936; MCCC1.

DR GK; Q96RQ3; -.

DR NIM; 210200; -.

DR GO; GO:0005759; C:mitochondrial matrix; NAS.

DR GO; GO:0009374; F:biotin binding; NAS.

DR GO; GO:0004485; F:methylcrotonyl-CoA carboxylase activity; NAS.

DR GO; GO:0006768; P:biotin metabolism; NAS.

DR GO; GO:0006552; P:leucine catabolism; NAS.

DR InterPro; IPR001882; Biotin_BS.

DR InterPro; IPR005482; Biotin_carb_C.

DR InterPro; IPR000089; Biotin_lipoyl.

DR InterPro; IPR005479; CPase_L_D2.

DR InterPro; IPR005481; CPase_L_N.

DR Pfam; PF02785; Biotin_carb_C; 1.

DR Pfam; PF00364; biotin_lipoyl; 1.

DR Pfam; PF00289; CPase_L chain; 1.

DR Pfam; PF02786; CPase_L_D2; 1.

DR PROSITE; PS00188; BIOTIN; 1.

DR PROSITE; PS00867; CPASE2; 1.

KW Mitochondrion; Ligase; Biotin; ATP-binding; Transit peptide;

KW Disease mutation; Polymorphism.

FT TRANSIT 1 47

FT CHAIN 48 725 METHYLCROTONYL-COA CARBOXYLASE ALPHA

FT CHAIN

FT NP_BIND 209 214 ATP (POTENTIAL).

FT ACT_SITE 339 339 BY SIMILARITY.

FT BINDING 681 681 BIOTIN (BY SIMILARITY).

FT DOMAIN 538 541 POLY-SER.

FT DOMAIN 713 718 POLY-GLU.

FT VARIANT 289 289 A -> V (in MCGI; mild form).

CC -!- PATHWAY: Gluconeogenesis.
CC -!- SUBUNIT: Homotetramer.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- INDUCTION: BY glucose.
CC -!- SIMILARITY: WITH OTHER BIOTIN CARBOXYLASES, LIPOAMIDE TRANSFERASES
CC AND CARBAMYL PHOSPHATE SYNTHETASES.
CC -----
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CC -----
DR EMBL; X59890; CAA42544.1; --
DR EMBL; Z36087; CAA85182.1; --
DR EMBL; U35647; AAC49147.1; --
DR PIR; S46094; S46094.
DR HSSP; P24182; IBNC.
DR GERMOnline; 138761; --
DR SGD; S0000422; PYC2.
DR GO; GO:0005829; C:cytosol; IDA.
DR GO; GO:0004736; F:pyruvate carboxylase activity; IDA.
DR InterPro; IPR001882; Biotin_BS.
DR InterPro; IPR005482; Biotin_carb_C.
DR InterPro; IPR000089; Biotin_lipoyl.
DR InterPro; IPR005479; CPase_L_D2.
DR InterPro; IPR005481; CPase_L_N.
DR InterPro; IPR000891; HMGL-like.
DR InterPro; IPR003379; PYC_OADA.
DR InterPro; IPR005930; Pyruv carbox.
DR Pfam; PF02785; Biotin_carb_C; 1.
DR Pfam; PF00364; biotin_lipoyl; 1.
DR Pfam; PF00289; CPase_L chain; 1.
DR Pfam; PF02786; CPase_L_D2; 1.
DR Pfam; PF00682; HMGL-like; 1.
DR Pfam; PF02436; PYC_OADA; 1.
DR TIGRFAMs; TIGR01235; pyruv carbox; 1.
DR PROSITE; PS00188; BIOTIN; 1.
DR PROSITE; PS00866; CPASE_1; 1.
DR PROSITE; PS00867; CPASE_2; 1.
KW Ligase; Multifunctional enzyme; Biotin; Gluconeogenesis; ATP-binding;
KW Zinc; Multigene family.
FT NP_BIND 183 188
FT ACT_SITE 313 313
FT BINDING 1136 1136
FT CONFLICT 15 15
FT CONFLICT 132 132
FT CONFLICT 238 238
FT CONFLICT 268 268
FT CONFLICT 546 546
FT CONFLICT 642 642
FT CONFLICT 771 773
FT CONFLICT 831 831
FT CONFLICT 839 839
FT CONFLICT 1001 1001
FT CONFLICT 1155 1155
FT CONFLICT 1178 1178
FT CONFLICT 1180 1180
FT CONFLICT 1180 1180
SQ SEQUENCE 1180 AA; 130166 MW; AD60DA3A60F5E001 CRC64;

Query Match 22.4%; Score 138; DB 1; Length 1180;
Best Local Similarity 38.5%; Pred. No. 0.0039;
Matches 25; Conservative 19; Mismatches 21; Indels 0; Gaps 0;

QY 55 EIPAPLAGTGVSKLVKSGDITVKGQTVKAGQTVLVLEAMKMETEINAPTQDKVKEVLVKERDAVQ 114
Db 1103 QIGAPMAGVIIIEVKVHKGSLVKKGESIAVLAMKMEMVSSPADGQVKDFIKDGESVDA 1162

QY 115 GQGLI 119
Db 1163 SLLV 1167

RESULT 14

BCCP CHLMU STANDARD; PRT; 163 AA.
AC Q9PKR5;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Biotin carboxyl carrier protein of acetyl-CoA carboxylase (BCCP).
GN ACCB OR TC0399.
OS Chlamydia muridarum.
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaeae; Chlamydia.
OX NCBI_TaxID=83560;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MoPn / Ni99;
RX MEDLINE=20150255; PubMed=10684935;
RA Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
RA White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S.,
RA Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,
RA Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.,
RA Eisen J., Fraser C.M.;
RT "Genome sequences of Chlamydia trachomatis MoPn and Chlamydia
RT pneumoniae AR39.";
RL Nucleic Acids Res. 28:1397-1406(2000).
CC -!- FUNCTION: This protein is a component of the acetyl coenzyme A
CC carboxylase complex; first, biotin carboxylase catalyzes the
CC carboxylation of the carrier protein and then the transcarboxylase
CC transfers the carboxyl group to form malonyl-CoA (By similarity).
CC -!- PATHWAY: Long-chain fatty acid biosynthesis; first step.
CC -!- SUBUNIT: Homodimer (By similarity).
CC -----
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CC -----
DR EMBL; AE002306; AAF39256.1; --
DR PIR; C81708; C81708.
DR HSSP; P02905; 1BDO.
DR TIGR; TC0399; --
DR InterPro; IPR001249; AcCoA biotinCC.
DR InterPro; IPR001882; Biotin_BS.
DR InterPro; IPR000089; Biotin_lipoyl.
DR Pfam; PF00364; biotin_lipoyl; 1.
DR PRINTS; PR01071; ACOABIOTINCC.
DR TIGRFAMs; TIGR00531; BCCP; 1.
DR PROSITE; PS00188; BIOTIN; 1.
KW Fatty acid biosynthesis; Biotin; Complete proteome.
FT BINDING 127 127 BIOTIN (BY SIMILARITY).
SQ SEQUENCE 163 AA; 18084 MW; 8536D58B5CE11D3B CRC64;

Query Match 21.7%; Score 133.5; DB 1; Length 163;
Best Local Similarity 29.8%; Pred. No. 0.0014;
Matches 42; Conservative 21; Mismatches 57; Indels 21; Gaps 4;

QY 2 KLKVTWNGTAYDVEDVDVKSHENPM--GTILFGGTGGAPAPA-----AGGAGA 48
Db 20 RIAIKRDGFELELRTDGTGNIQEPVYFNRLFAGFTQERPIPSDQNLGNPIVKEVGEKKE 79
QY 49 GKAGEGE-IPAPLAGTV-----SKILVKEGDTVKAGQTVLVLEAMKMETEINAPTQDK 100
Db 80 DKPVEGDFIVSPLVGTFFYGAPSPESPAFVKPGDIVSEDTVCIVEAMKVMNEVKAGMAGR 139
QY 101 VEKVLVKERDAVQGGQGLIKI 121
Db 140 VEEVLITNGDPVQFGSKLFRI 160


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RESULT 15
PYC1_YEAST
ID PYC1_YEAST STANDARD; PRT; 1178 AA.
AC P11154;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Pyruvate carboxylase 1 (EC 6.4.1.1) (Pyruvic carboxylase 1) (PCB 1).
GN PYC1 OR PYV OR YGL062W.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
RN [1];
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX MEDLINE=88298805; PubMed=3042770;
RA Lim F., Morris C.P., Occhiodoro F., Wallace J.C.;
RT "Sequence and domain structure of yeast pyruvate carboxylase.";
RL J. Biol. Chem. 263:11493-11497(1988).
RN [2];
RP SEQUENCE FROM N.A.
RC STRAIN=S288C;
RX MEDLINE=97377993; PubMed=9234674;
RA Feuermann M., de Montigny J., Potier S., Souciet J.-L.;
RT "The characterization of two new clusters of duplicated genes
RT suggests a 'Lego' organization of the yeast Saccharomyces cerevisiae
RT chromosomes.";
RL Yeast 13:861-869(1997).
RN [3];
RP SEQUENCE OF 1003-1178 FROM N.A.
RX MEDLINE=87241529; PubMed=3036126;
RA Morris C.P., Lim F., Wallace J.C.;
RT "Yeast pyruvate carboxylase: gene isolation.";
RL Biochem. Biophys. Res. Commun. 145:390-396(1987).
CC -!- FUNCTION: Pyruvate carboxylase catalyzes a 2-step reaction,
CC involving the ATP-dependent carboxylation of the covalently
CC attached biotin in the first step and the transfer of the
CC carboxyl group to pyruvate in the second.
CC -!- CATALYTIC ACTIVITY: ATP + pyruvate + HCO(3) (-) = ADP + phosphate +
CC oxaloacetate.
CC -!- COFACTOR: Biotin and zinc.
CC -!- PATHWAY: Gluconeogenesis.
CC -!- SUBUNIT: Homotetramer.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: WITH OTHER BIOTIN CARBOXYLASES, LIPOAMIDE TRANSFERASES
CC AND CARBAMYL PHOSPHATE SYNTHETASES.
-----
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CC or send an email to license@isb-sib.ch).
-----
DR EMBL; J03889; AAA34843.1; -
DR EMBL; Z72584; CAA96765.1; -
DR PIR; S64066; QYBYP.
DR HSSP; P24182; 1BNC.
DR GernOnline; 141110; -.
DR SGD; S0003030; PYC1.
DR GO; GO:0005829; C:cytosol; IDA.
DR GO; GO:0004736; F:pyruvate carboxylase activity; IDA.
DR InterPro; IPR001882; Biotin_BS.
DR InterPro; IPR005482; Biotin_carb_C.
DR InterPro; IPR000089; Biotin_lipoYL.
DR InterPro; IPR005479; CPase_I_D2.
DR InterPro; IPR005481; CPase_L_N.
DR InterPro; IPR000891; HMGL-Like.
DR InterPro; IPR003379; PYC_OADA.
DR InterPro; IPR005930; Pyruv_carbox.
DR Pfam; PF02785; Biotin_carb_C; 1.
DR Pfam; PF00364; biotin_lipoYL; 1.
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DR Pfam; PF00289; CPSase_L_chain; 1.
DR Pfam; PF02786; CPSase_L_D2; 1.
DR Pfam; PF00682; HMGL-Like; 1.
DR Pfam; PF02436; PYC_OADA; 1.
DR TIGRFAMs; TIGR01235; pyruv carbox; 1.
DR PROSITE; PS00188; BIOTIN; 1.
DR PROSITE; PS00866; CPSASE_1; 1.
DR PROSITE; PS00867; CPSASE_2; 1.
KW Ligase; Multifunctional enzyme; Biotin; Gluconeogenesis; ATP-binding;
KW Zinc; Multigene family.
FT NP_BIND 182 187 ATP (POTENTIAL).
FT ACT_SITE 312 312 BY SIMILARITY.
FT BINDING 1135 1135 BIOTIN (BY SIMILARITY).
FT CONFLICT 462 462 T -> G (IN REF. 1).
FT CONFLICT 493 493 V -> D (IN REF. 1).
FT CONFLICT 595 595 R -> A (IN REF. 1).
FT CONFLICT 619 619 E -> Q (IN REF. 1).
FT CONFLICT 664 664 G -> S (IN REF. 1).
FT CONFLICT 772 772 A -> R (IN REF. 1).
FT CONFLICT 879 879 E -> Q (IN REF. 1).
FT CONFLICT 909 909 Q -> K (IN REF. 1).
SQ SEQUENCE 1178 AA; 130099 MW; BC7110A8AFB23E04 CRC64;

Query Match 21.6%; Score 133; DB 1; Length 1178;
Best Local Similarity 42.2%; Pred. No. 0.0092;
Matches 27; Conservative 15; Mismatches 22; Indels 0; Gaps 0;

QY 56 IPAPLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVKVVKERDAVQGG 115
DB 1103 IGAPMAGVIVEVKVHKGSLIKKQGPVAVLSAMKMEMIISPSDQGVKEVSDGENVDSS 1162
QY 116 QGLI 119
DB 1163 DLLV 1166

RESULT 16
PYC_PICPA
ID PYC_PICPA STANDARD; PRT; 1189 AA.
AC P78992;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Pyruvate carboxylase (EC 6.4.1.1) (Pyruvic carboxylase) (PCB).
GN PYC1.
OS Pichia pastoris (Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Pichia.
OX NCBI_TaxID=4922;
RN [1];
RP SEQUENCE FROM N.A.
RX MEDLINE=98301182; PubMed=9639311;
RA Menendez J., Delgado J., Gancedo C.;
RT "Isolation of the Pichia pastoris PYC1 gene encoding pyruvate
RT carboxylase and identification of a suppressor of the pyv
RT phenotype.";
RL Yeast 14:647-654(1998).
CC -!- FUNCTION: Pyruvate carboxylase catalyzes a 2-step reaction,
CC involving the ATP-dependent carboxylation of the covalently
CC attached biotin in the first step and the transfer of the
CC carboxyl group to pyruvate in the second (By similarity).
CC -!- CATALYTIC ACTIVITY: ATP + pyruvate + HCO(3) (-) = ADP + phosphate +
CC oxaloacetate.
CC -!- COFACTOR: Biotin and zinc.
CC -!- PATHWAY: Gluconeogenesis.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: WITH OTHER BIOTIN CARBOXYLASES, LIPOAMIDE TRANSFERASES
CC AND CARBAMYL PHOSPHATE SYNTHETASES.
-----
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```


RC STRAIN=K12 / EMG2;
RX MEDLINE=97443975; PubMed=9298646;
RA Link A.J., Robison K., Church G.M.;
RT "Comparing the predicted and observed properties of proteins encoded
in the genome of Escherichia coli K-12";
RL Electrophoresis 18:1259-1313(1997).
RN [4]
RP SEQUENCE OF 34-46.
RX MEDLINE=84256520; PubMed=6821375;
RA Hale G., Perham R.N.;
RT "Amino acid sequence around lipoid acid residues in the pyruvate
dehydrogenase multienzyme complex of Escherichia coli.";
RL Biochem. J. 187:905-908(1980).
RN [5]
RP MUTAGENESIS OF HIS-602.
RX MEDLINE=90351365; PubMed=2201286;
RA Russel G.C., Guest J.R.;
RT "Overexpression of restructured pyruvate dehydrogenase complexes and
site-directed mutagenesis of a potential active-site histidine
residue.";
RL Biochem. J. 269:443-450(1990).
RN [6]
RP LIPOYLATED DOMAINS STUDIES.
RX MEDLINE=91024917; PubMed=2121129;
RA Ali S.T., Guest J.R.;
RT "Isolation and characterization of lipoylated and unlipoylated
domains of the E2p subunit of the pyruvate dehydrogenase complex of
Escherichia coli";
RL Biochem. J. 271:139-145(1990).
CC -!- FUNCTION: The pyruvate dehydrogenase complex catalyzes the overall
conversion of pyruvate to acetyl-CoA and CO(2). It contains
multiple copies of three enzymatic components: pyruvate
dehydrogenase (E1), dihydrolipoamide acetyltransferase (E2) and
lipoamide dehydrogenase (E3).
CC -!- CATALYTIC ACTIVITY: Acetyl-CoA + dihydrolipoamide = CoA + S-
acetyldihydrolipoamide.
CC -!- COFACTOR: Contains 3 covalently bound lipoyl cofactors.
CC -!- SUBUNIT: Forms a 24-polypeptide structural core with octahedral
symmetry.
CC -!- SIMILARITY: Belongs to the 2-oxoacid dehydrogenase family.
CC -!- SIMILARITY: Contains 3 lipoyl-binding domains.
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or send an email to license@isb-sib.ch).
CC -----
DR EMBL; V01498; CAA24741.1; -;
DR EMBL; D26562; BAB96685.1; -;
DR EMBL; AE000120; AAC73226.1; -;
DR PIR; A30278; XXECDP.
DR PDB; 1QJO; 21-JUL-00.
DR SWISS-2DPAGE; P06959; COLI.
DR ECO2DBASE; C062.7; 6TH EDITION.
DR ECO2DBASE; C070.0; 6TH EDITION.
DR EcoGene; EG10025; aceF.
DR InterPro; IPR001078; 2Oxoacid_dh.
DR InterPro; IPR006256; AceF.
DR InterPro; IPR000089; Biotin lipoyl.
DR InterPro; IPR004167; E3 binding.
DR InterPro; IPR003016; Lipoyl_BS.
DR Pfam; PF00198; 2-oxoacid_dh; 1.
DR Pfam; PF00364; biotin_lipoyl; 3.
DR Pfam; PF02817; e3 binding; 1.
DR ProDom; PD001115; 2Oxoacid_dh; 1.
DR TIGRFAMs; TIGR01348; PDHac_trf_long; 1.
DR PROSITE; PS00189; LIPOYL; 3.
KW Glycolysis; Transferase; Acyltransferase; Repeat; Lipoyl;
KW Complete proteome; 3D-structure.
FT INIT_MET 0

FT DOMAIN 1 314 LIPOYL BINDING, ACIDIC.
FT DOMAIN 316 629 SUBUNIT BINDING, CATALYTIC.
FT DOMAIN 372 388 HYDROPHOBIC.
FT DOMAIN 541 566 HYDROPHOBIC.
FT BINDING 40 40 LIPOYL.
FT BINDING 143 143 LIPOYL.
FT BINDING 244 244 LIPOYL.
FT ACT_SITE 546 546 POTENTIAL.
FT ACT_SITE 602 602 POTENTIAL.
FT REPEAT 1 102
FT REPEAT 103 203
FT REPEAT 204 313
FT MUTAGEN 602 602
SQ SEQUENCE 629 AA; 65964 MW; 058751268B2CCCC0 CRC64;
H->C: ABOLISHES CATALYTIC ACTIVITY.
Query Match 21.1%; Score 130; DB 1; Length 629;
Best Local Similarity 31.6%; Pred. No. 0.0086;
Matches 43; Conservative 20; Mismatches 53; Indels 20; Gaps 4;
QY 1 MKLKVTVNGTAYDVVDV-DKSHENPMGTILFGGTGAPAPAAAGGAGAGAGGAGGELPAP 59
|::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
146 MEVPAPFAGTVKEIKVNVGDKVSTGSLIMVFEVAGEAGAAAPAAKQEAAPAA-----PAP 201
QY 60 LAGT-----VSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTGDGKVEKVL 105
|::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
202 AAGVKEVNVDPDIGGDEVEVEMVKGDKVAAEQSLITVEGDKASMEVPAPFAGVVKELK 261
QY 106 VKERDAVQGGQGLIKI 121
|::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
262 VNVGDKVKTG-SLIMI 276
RESULT 19
MCCA SOYBN STANDARD; PRT; 731 AA.
AC Q42777; Q42778;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Methylcrotonyl-CoA carboxylase alpha chain, mitochondrial precursor
DE (EC 6.4.1.4) (3-Methylcrotonyl-CoA carboxylase 1) (MCCase alpha
subunit) (3-methylcrotonyl-CoA:carbon dioxide ligase alpha subunit).
GN MCCA.
OS Glycine max (Soybean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eucosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
OX NCBI_TaxID=3847;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF N-TERMINUS.
RC STRAIN=cv. Corsoy 79; TISSUE=Cotyledon;
RX MEDLINE=94286521; PubMed=8016064;
RA Song J., Wurtele E.S., Nikolau B.J.;
RT "Molecular cloning and characterization of the cDNA coding for the
biotin-containing subunit of 3-methylcrotonyl-CoA carboxylase:
RT identification of the biotin carboxylase and biotin-carrier
domains.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:5779-5783(1994).
CC -!- CATALYTIC ACTIVITY: ATP + 3-methylcrotonyl-CoA + HCO(3) (-) = ADP +
phosphate + 3-methylglutaconyl-CoA.
CC -!- COFACTOR: Biotin.
CC -!- PATHWAY: Leucine catabolism.
CC -!- SUBUNIT: Probably a heterodimer composed of biotin-containing
alpha subunits and beta subunits (By similarity).
CC -!- SUBCELLULAR LOCATION: Mitochondrial matrix.
CC -!- TISSUE SPECIFICITY: In leaves, cotyledons and stems.
CC -----
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RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrenner P.,
RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
RA Garber R.L., Goltzy L., Tolentino E., Westbrook-Wadman S., Yuan Y.,
RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Reizer J., Saler M.H., Hancock R.E.W., Lory S., Olson M.V.;
RT "Complete genome sequence of Pseudomonas aeruginosa PAO1, an
RT opportunistic pathogen.";
RL Nature 406:959-964(2000).
CC -!- FUNCTION: The pyruvate dehydrogenase complex catalyzes the overall
CC conversion of pyruvate to acetyl-CoA and CO(2). It contains
CC multiple copies of three enzymatic components: pyruvate
CC dehydrogenase (E1), dihydrolipoamide acetyltransferase (E2) and
CC lipoamide dehydrogenase (E3).
CC -!- CATALYTIC ACTIVITY: Acetyl-CoA + dihydrolipoamide = CoA + S-
CC acetyldihydrolipoamide.
CC -!- COFACTOR: Contains 2 covalently bound lipoyl cofactors (By
CC similarity).
CC -!- SUBUNIT: Forms a 24-polypeptide structural core with octahedral
CC symmetry.
CC -!- SIMILARITY: Belongs to the 2-oxoacid dehydrogenase family.
CC -!- SIMILARITY: Contains 2 lipoyl-binding domains.
CC -----
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CC -----
DR EMBL; U47920; AAC45354.1; --.
DR EMBL; AE004914; AAG08401.1; --.
DR PIR; H83018; H83018.
DR HSSP; P10802; 1EAF.
DR InterPro; IPR001078; 2Oxoacid_dh.
DR InterPro; IPR006256; AceF.
DR InterPro; IPR000089; Biotin_lipoyl.
DR InterPro; IPR004167; E3_binding.
DR InterPro; IPR003016; Lipoyl_BS.
DR Pfam; PF00198; 2-oxoacid_dh; 1.
DR Pfam; PF00364; biotin_lipoyl; 2.
DR Pfam; PF02817; e3_binding; 1.
DR ProDom; PD001115; 2Oxoacid_dh; 1.
DR TIGRFAMs; TIGR01348; PDHac_trf_long; 1.
DR PROSITE; PS00189; LIPOYL; 2.
KW Glycolysis; Transferase; Acyltransferase; Repeat; Lipoyl;
KW Complete proteome.
FT BINDING 41 41 LIPOYL (BY SIMILARITY).
FT BINDING 159 159 LIPOYL (BY SIMILARITY).
FT ACT SITE 520 520 POTENTIAL.
FT CONFLICT 225 225 A -> V (IN REF. 1).
FT CONFLICT 295 301 GGAGATG -> AVPAPR (IN REF. 1).
FT CONFLICT 328 329 MQ -> IE (IN REF. 1).
SQ SEQUENCE 547 AA; 56709 MW; 24E15CC9A590CB4 CRC64;

Query Match 21.0%; Score 129; DB 1; Length 547;
Best Local Similarity 37.0%; Pred. No. 0.009;
Matches 34; Conservative 15; Mismatches 35; Indels 8; Gaps 2;

QY 38 APAPA---AGGAGAGKAGEGEIPAPLAGTVSK-----ILVKEGDTVKAGQTVLVLEAMKM 89
Db 101 APAPAPSESKPAPAPAAASVDIKVPDIGSAGKANVIEVMVKAGDTVEADQSLTLESCKA 160

QY 90 ETEINAPTQKVEKVLVKERDAVQGGQGLIKI 121
Db 161 SMEIPSPASGVVESVSIKVGDEVTGDLILKL 192

RESULT 22
PYC MOUSE
ID PYC_MOUSE STANDARD; PRT; 1178 AA.
AC Q05920;

DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Pyruvate carboxylase, mitochondrial precursor (EC 6.4.1.1) (Pyruvic
DE carboxylase) (PCB).
GN PC OR PCX.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Adipocyte;
RX MEDLINE=93189578; PubMed=8446588;
RA Zhang J., Xia W.L., Brew K., Ahmad F.;
RT "Adipose pyruvate carboxylase: amino acid sequence and domain
RT structure deduced from cDNA sequencing.";
RL Proc. Natl. Acad. Sci. U.S.A. 90:1766-1770(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Liver;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettaman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: Pyruvate carboxylase catalyzes a 2-step reaction,
CC involving the ATP-dependent carboxylation of the covalently
CC attached biotin in the first step and the transfer of the
CC carboxyl group to pyruvate in the second. Catalyzes in a tissue
CC specific manner, the initial reactions of glucose (liver, kidney)
CC and lipid (adipose tissue, liver, brain) synthesis from pyruvate.
CC -!- CATALYTIC ACTIVITY: ATP + pyruvate + HCO(3) (-) = ADP + phosphate +
CC oxaloacetate.
CC -!- COFACTOR: Biotin and manganese.
CC -!- PATHWAY: Gluconeogenesis and lipogenesis.
CC -!- SUBUNIT: Homotetramer.
CC -!- SUBCELLULAR LOCATION: Mitochondrial matrix.
CC -!- TISSUE SPECIFICITY: Liver, kidney, adipose tissue, liver and
CC brain.
CC -!- SIMILARITY: WITH OTHER BIOTIN CARBOXYLASES, LIPOAMIDE TRANSFERASES
CC AND CARBAMYL PHOSPHATE SYNTHETASES.
CC -----
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CC -----
DR EMBL; L09192; AAA39737.1; --.
DR EMBL; BC055030; AAH55030.1; --.
DR PIR; A47255; A47255.
DR HSSP; P24182; 1BNC.
DR SWISS-2DPAGE; Q05920; MOUSE.
DR MGD; MGI:97520; Pcx.


```
DR InterPro; IPR001882; Biotin_BS.
DR InterPro; IPR005482; Biotin_carb_C.
DR InterPro; IPR000089; Biotin_lipoyl.
DR InterPro; IPR005479; CPase_L_D2.
DR InterPro; IPR005481; CPase_L_N.
DR InterPro; IPR000891; HMGL-like.
DR InterPro; IPR003379; PYC_OADA.
DR InterPro; IPR005930; Pyruv_carbox.
DR Pfam; PF02785; Biotin_carb_C; 1.
DR Pfam; PF00364; biotin_lipoyl; 1.
DR Pfam; PF00289; CPase_L_chain; 1.
DR Pfam; PF02786; CPase_L_D2; 1.
DR Pfam; PF00682; HMGL-like; 1.
DR Pfam; PF02436; PYC_OADA; 1.
DR TIGRFAMs; TIGR01235; pyruv_carbox; 1.
DR PROSITE; PS00188; BIOTIN; 1.
KW Ligase; Multifunctional enzyme; Biotin; Manganese; Gluconeogenesis;
KW ATP-binding; Mitochondrion; Lipid synthesis; Transit peptide.
FT TRANSIT 1 20 MITOCHONDRION (POTENTIAL).
FT CHAIN 21 1178 PYRUVATE CARBOXYLASE.
FT DOMAIN 21 549 BIOTIN CARBOXYLASE (BY SIMILARITY).
FT DOMAIN 550 1000 CARBOXYLTRANSFERASE (BY SIMILARITY).
FT DOMAIN 1096 1178 BIOTIN CARBOXYL CARRIER PROTEIN
(BY SIMILARITY).
FT NP BIND 198 203 ATP (BY SIMILARITY).
FT ACT SITE 328 328 BY SIMILARITY.
FT BINDING 1144 1144 BIOTIN (BY SIMILARITY).
FT SEQUENCE 1178 AA; 129684 MW; 14CEA0F9DA8B8127 CRC64;
SQ

Query Match 21.0%; Score 129; DB 1; Length 1178;
Best Local Similarity 40.6%; Pred. No. 0.018;
Matches 28; Conservative 14; Mismatches 27; Indels 0; Gaps 0;

QY 53 EGEIPAPLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTQKVEKVLVKERDAV 112
Db 1109 KGQICAPMGKVIDIKVAAGDKVAKGQPLCVLSAMKMETVVTSPMEGTIRKVVHTKDMTL 1168

QY 113 QGGQGLIKI 121
Db 1169 EGGDLILEI 1177

RESULT 23
ODP2_ACHLA STANDARD; PRT; 544 AA.
AC P35489;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Dihydrolipoamide acetyltransferase component of pyruvate dehydrogenase
DE complex (EC 2.3.1.12) (E2).
GN PDHC.
OS Acholeplasma laidlawii.
OC Bacteria; Firmicutes; Mollicutes; Acholeplasmatales;
OC Acholeplasmataceae; Acholeplasma.
OX NCBI_TaxID=2148;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX MEDLINE=92138635; PubMed=1735725;
RA Wallbrandt P., Tegman V., Jonsson B.-H., Wieslander A.;
RT "Identification and analysis of the genes coding for the putative
RT pyruvate dehydrogenase enzyme complex in Acholeplasma laidlawii.";
RL J. Bacteriol. 174:1388-1396(1992).
CC -!- FUNCTION: The pyruvate dehydrogenase complex catalyzes the overall
CC conversion of pyruvate to acetyl-CoA and CO(2). It contains
CC multiple copies of three enzymatic components: pyruvate
CC dehydrogenase (E1), dihydrolipoamide acetyltransferase (E2) and
CC lipoamide dehydrogenase (E3).
CC -!- CATALYTIC ACTIVITY: Acetyl-CoA + dihydrolipoamide = CoA + S-
CC acetyldihydrolipoamide.
CC -!- COFACTOR: Contains 2 covalently bound lipoyl cofactors
CC (Potential).
CC -!- SUBUNIT: Forms a 24-polypeptide structural core with octahedral
```

```
CC symmetry (By similarity).
CC -!- SIMILARITY: Belongs to the 2-oxoacid dehydrogenase family.
CC -!- SIMILARITY: Contains 2 lipoyl-binding domains.
CC
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; M81753; AAA21909.1; -.
DR PIR; C42653; C42653.
DR HSSP; P07016; 1C4T.
DR InterPro; IPR001078; 2Oxoacid dh.
DR InterPro; IPR000089; Biotin_lipoyl.
DR InterPro; IPR004167; E3_binding.
DR InterPro; IPR003016; Lipoyl_BS.
DR Pfam; PF00198; 2-oxoacid dh; 1.
DR Pfam; PF00364; biotin_lipoyl; 2.
DR Pfam; PF02817; e3_binding; 1.
DR ProDom; PD001115; 2Oxoacid dh; 1.
DR PROSITE; PS00189; LIPOYL; 2.
KW Glycolysis; Transferase; Acyltransferase; Lipoyl.
FT BINDING 42 42 LIPOYL (BY SIMILARITY).
FT BINDING 154 154 LIPOYL (BY SIMILARITY).
FT ACT SITE 516 516 POTENTIAL.
FT SEQUENCE 544 AA; 57261 MW; 81E92D869CFD5424 CRC64;
SQ

Query Match 20.8%; Score 128; DB 1; Length 544;
Best Local Similarity 29.0%; Pred. No. 0.011;
Matches 42; Conservative 23; Mismatches 54; Indels 26; Gaps 4;

QY 2 KLVTVNGTAYDVVDVDKSHENPMGTILF-----GGGTGGA-----PAPAAGGA 46
Db 46 ELPSVDGTI--VSLGAKEGEEIHVGQIIIVTIDGTGTPAAAPAPAQVSAPTAPAAAPQ 103

QY 47 GAGKAGEGEI-----PAPLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPT 97
Db 104 VAAPAASGDIYDFKADIGEGIHGEGITLQWNFKVGVKVEGETLVVVETDKVNAELPSPV 163

QY 98 DGKVEKVLVKERDAVGGQGLIKIG 122
Db 164 DGTILKLGKAGEGEVIHVGTVVLIG 188

RESULT 24
BCCA_MYCTU
ID BCCA_MYCTU STANDARD; PRT; 654 AA.
AC P46401;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Acetyl-/propionyl-coenzyme A carboxylase alpha chain [Includes: Biotin
DE carboxylase (EC 6.3.4.14); Biotin carboxyl carrier protein (BCCP)].
GN ACCA1 OR BCCA OR RV2501C OR MT2576 OR MTCY07A7.07C OR MB2529C.
OS Mycobacterium tuberculosis, and
OS Mycobacterium bovis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1773, 1765;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=M.tuberculosis; STRAIN=Isolate 50410;
RX MEDLINE=94222829; PubMed=7909542;
RA Norman E., de Smet K.A.L., Stoker N.G., Ratledge C., Wheeler P.R.,
RA Dale J.W.;
RT "Lipid synthesis in mycobacteria: characterization of the biotin
RT carboxyl carrier protein genes from Mycobacterium leprae and M.
RT tuberculosis.";
RL J. Bacteriol. 176:2525-2531(1994).
RN [2]
```


RP SEQUENCE FROM N.A.
RC SPECIES=M.tuberculosis; STRAIN=H37Rv;
RX MEDLINE=98295987; PubMed=9634230;
RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
RA Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekai F.,
RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
RA Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
RA Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
RT "Deciphering the biology of Mycobacterium tuberculosis from the
RT complete genome sequence.";
RL Nature 393:537-544(1998).
RN [3]
RP SEQUENCE FROM N.A.
RC SPECIES=M.tuberculosis; STRAIN=CDC 1551 / Oshkosh;
RX MEDLINE=22206494; PubMed=12218036;
RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
RA Peterson J., DeBoy R., Dodson R., Gwinn M., Haft D., Hickey E.,
RA Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg S.L.,
RA Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
RA Bishai W., Jacobs W.R. Jr., Venter J.C., Fraser C.M.;
RT "Whole-genome comparison of Mycobacterium tuberculosis clinical and
RT laboratory strains.";
RL J. Bacteriol. 184:5479-5490(2002).
RN [4]
RP SEQUENCE FROM N.A.
RC SPECIES=M.bovis; STRAIN=AF2122/97;
RX MEDLINE=22709107; PubMed=12788972;
RA Garnier T., Eiglmeier K., Camus J.-C., Medina N., Mansoor H.,
RA Pryor M., Duthoy S., Grondin S., Lacroix C., Monsempe C., Simon S.,
RA Harris B., Atkin R., Doggett J., Mayes R., Keating L., Wheeler P.R.,
RA Parkhill J., Barrell B.G., Cole S.T., Gordon S.V., Hewinson R.G.;
RT "The complete genome sequence of Mycobacterium bovis.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:7877-7882(2003).
CC -!- FUNCTION: THIS PROTEIN CARRIES TWO FUNCTIONS: BIOTIN CARBOXYL
CC CARRIER PROTEIN AND BIOTIN CARBOXYLTRANSFERASE.
CC -!- CATALYTIC ACTIVITY: ATP + biotin-carboxyl-carrier protein + CO(2)
CC = ADP + phosphate + carboxybiotin-carboxyl-carrier protein.
CC -!- COFACTOR: Biotin.
CC -!- PATHWAY: Long-chain fatty acid biosynthesis; first step.
CC -!- SUBUNIT: MULTIMER COMPRISED OF 2 DIFFERENT SUBUNITS, THE LARGER
CC ONE (63/64 kDa) HAS BIOTIN CARBOXYLASE AND BIOTIN CARRIER
CC FUNCTIONS, WHILE THE SMALLER SUBUNIT POSSESSES CARBOXYLTRANSFERASE
CC AND SUBSTRATE BINDING ACTIVITY.
CC -!- SIMILARITY: TO OTHER BIOTIN-DEPENDENT ENZYMES AND CARBAMOYL-
CC PHOSPHATE SYNTHETASES.

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DR EMBL; Z19549; CAA79609.1; -.
DR EMBL; Z95556; CAB08919.1; -.
DR EMBL; AE007094; AAK46880.1; -.
DR EMBL; BX248342; CAD97390.1; -.
DR PIR; B55579; B55579.
DR HSSP; P24182; 1BNC.
DR TIGR; MT2576; -.
DR TubercuList; RV2501c; -.
DR InterPro; IPR001882; Biotin_BS.
DR InterPro; IPR005482; Biotin_carb_C.
DR InterPro; IPR000089; Biotin_lipoyl.
DR InterPro; IPR005479; CPase_L_D2.
DR InterPro; IPR005481; CPase_L_N.
DR Pfam; PF02785; Biotin_carb_C; 1.
DR Pfam; PF00364; biotin_lipoyl; 1.
DR Pfam; PF00289; CPSase_L_chain; 1.

DR Pfam; PF02786; CPSase_L_D2; 1.
DR PROSITE; PS00188; BIOTIN; 1.
DR PROSITE; PS00866; CPSASE_1; 1.
DR PROSITE; PS00867; CPSASE_2; 1.
KW Fatty acid biosynthesis; Ligase; Biotin; Multifunctional enzyme;
KW ATP-binding; Complete proteome.
FT DOMAIN 1 437 BIOTIN CARBOXYLASE.
FT DOMAIN 588 654 BIOTIN CARBOXYL CARRIER PROTEIN.
FT NP_BIND 162 167 ATP (BY SIMILARITY).
FT ACT_SITE 294 294 BY SIMILARITY.
FT BINDING 620 620 BIOTIN (BY SIMILARITY).
SQ SEQUENCE 654 AA; 70592 MW; FAA0A1A46432CABF CRC64;
Query Match 20.4%; Score 125.5; DB 1; Length 654;
Best Local Similarity 40.8%; Pred. No. 0.019;
Matches 29; Conservative 14; Mismatches 27; Indels 1; Gaps 1;
QY 51 AGEGETPAPLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTGDGKVEKLVKERD 110
Db 583 ARPAEVVSPMPGSVIAVQVESGQISAGDVVVVVEAMKMEHSLAPVSGRVQ-VLVSVGD 641
QY 111 AVQGGQGLIKI 121
Db 642 QVKVEQVLARI 652
RESULT 25
ODP2 AZOVI STANDARD; PRT; 637 AA.
AC P10802;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Dihydropolipoamide acetyltransferase component of pyruvate dehydrogenase
DE complex (EC 2.3.1.12) (E2).
OS Azotobacter vinelandii.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Azotobacter.
OX NCBI_TaxID=354;
RN [1] SEQUENCE FROM N.A.
RC STRAIN=ATCC 478;
RX MEDLINE=88271330; PubMed=3292237;
RA Hanemaaijer R., Janssen A., de Kok A., Veeger C.;
RT "The dihydropolipoamide acetyltransferase component of the pyruvate
RT dehydrogenase complex from Azotobacter vinelandii. Molecular cloning
RT and sequence analysis.";
RL Eur. J. Biochem. 174:593-599(1988).
RN [2]
RP SEQUENCE OF 1-15 AND 380-415.
RX MEDLINE=88082750; PubMed=3691494;
RA Hanemaaijer R., de Kok A., Jolles J., Veeger C.;
RT "The domain structure of the dihydropolipoamide acetyltransferase component
RT of the pyruvate dehydrogenase complex from Azotobacter vinelandii.";
RL Eur. J. Biochem. 169:245-252(1987).
RN [3]
RP LIPOYL DOMAIN CONFORMATION.
RX MEDLINE=89052887; PubMed=3191993;
RA Hanemaaijer R., Vervoort J., Westphal A.H., de Kok A., Veeger C.;
RT "Mobile sequences in the pyruvate dehydrogenase complex, the E2
RT component, the catalytic domain and the 2-oxoglutarate dehydrogenase
RT complex of Azotobacter vinelandii, as detected by 600 MHz 1H-NMR
RT spectroscopy.";
RL FEBS Lett. 240:205-210(1988).
RN [4]
RX X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF 381-637.
RP MEDLINE=92196586; PubMed=1549782;
RA Mattevi A., Obmolova G., Schulze E., Kalk K.H., Westphal A.H.,
RA de Kok A., Hol W.G.J.;
RT "Atomic structure of the cubic core of the pyruvate dehydrogenase
RT multienzyme complex.";
RL Science 255:1544-1550(1992).
RN [5]

RP SEQUENCE FROM N.A.
RC STRAIN=H16 / DSM 428 / ATCC 17699;
RX MEDLINE=94292470; PubMed=8021225;
RA Hein S., Steinbuechel A.;
RT "Biochemical and molecular characterization of the Alcaligenes
RT eutrophus pyruvate dehydrogenase complex and identification of a new
RT type of dihydrolipoamide dehydrogenase.";
RL J. Bacteriol. 176:4394-4408(1994).
CC -!- FUNCTION: The pyruvate dehydrogenase complex catalyzes the overall
CC conversion of pyruvate to acetyl-CoA and CO(2). It contains
CC multiple copies of three enzymatic components: pyruvate
CC dehydrogenase (E1), dihydrolipoamide acetyltransferase (E2) and
CC lipoamide dehydrogenase (E3).
CC -!- CATALYTIC ACTIVITY: Acetyl-CoA + dihydrolipoamide = CoA + S-
CC acetyldihydrolipoamide.
CC -!- COFACTOR: Contains 2 covalently bound lipoyl cofactors (By
CC similarity).
CC -!- SUBUNIT: Forms a 24-polypeptide structural core with octahedral
CC symmetry.
CC -!- SIMILARITY: Belongs to the 2-oxoacid dehydrogenase family.
CC -!- SIMILARITY: Contains 2 lipoyl-binding domains.
CC -----
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CC -----
CC EMBL; U09865; AAA21599.1; ..
CC PIR; B55514; B55514.
CC HSSP; P10802; 1DPC.
CC InterPro; IPR001078; 2Oxoacid_dh.
CC InterPro; IPR006256; AceF.
CC InterPro; IPR000089; Biotin_lipoyl.
CC InterPro; IPR003016; Lipoyl_BS.
CC InterPro; IPR00198; 2-oxoacid_dh.
CC Pfam; PF00364; biotin_lipoyl; 2.
CC Pfam; PF00115; 2Oxoacid_dh; 1.
CC ProDom; PD00115; 2Oxoacid_dh; 1.
CC TIGRFAMs; TIGR01348; PDHac_trf_long; 1.
CC PROSITE; PS00189; LIPOYL; 2.
CC Glycolysis; Transferase; Acyltransferase; Repeat; Lipoyl.
KW BINDING 44 44 LIPOYL (BY SIMILARITY).
FT BINDING 162 162 LIPOYL (BY SIMILARITY).
FT ACT SITE 526 526 POTENTIAL.
SQ SEQUENCE 553 AA; 57338 MW; BF5D370CC60C3F12 CRC64;

Query Match 19.8%; Score 122; DB 1; Length 553;
Best Local Similarity 38.9%; Pred. No. 0.03;
Matches 35; Conservative 12; Mismatches 35; Indels 8; Gaps 2;

QY 38 APAPAGGAGAGKAGEG---EIPAPLAG-----TVSKILVKEGDTVKAGQTVLVLEAMKM 89
Db 104 APAPAAAPAAAPAGGGGTIEVKVPDIDGYDAPVIEVHVKAGDTINAEADVTTLES DKA 163

QY 90 ETEINAPTQKVEKVLVKERDAVQGGQLI 119
Db 164 TMDVPSQGGVGVKVKVGDNVAEGLLL 193

RESULT 27
PYC HUMAN
ID - PYC HUMAN STANDARD; PRT; 1178 AA.
AC P11498; Q16705;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Pyruvate carboxylase, mitochondrial precursor (EC 6.4.1.1) (Pyruvic
DE carboxylase) (PCB).
GN PC.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney, and Liver;
RX MEDLINE=95002202; PubMed=7918683;
RA Wexler I.D., Du Y., Lisgaris M.V., Mandal S.K., Freytag S.O.,
RA Yang B.-S., Liu T.-C., Kwon M., Patel M.S., Kerr D.S.;
RT "Primary amino acid sequence and structure of human pyruvate
RT carboxylase.";
RL Biochim. Biophys. Acta 1227:46-52(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=94324922; PubMed=8048912;
RA Mackay N., Rigat B., Douglas C., Chen H.S., Robinson B.H.;
RT "cDNA cloning of human kidney pyruvate carboxylase.";
RL Biochem. Biophys. Res. Commun. 202:1009-1014(1994).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney, and Liver;
RA Walker M.E., Jitrapakdee S., Val D.L., Wallace J.C.;
RL Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Prange C.,
RA Brownstein M.J., Udgin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [5]
RP SEQUENCE OF 1083-1178 FROM N.A.
RX MEDLINE=87212051; PubMed=3555348;
RA Lamhonwah A.-M., Quan F., Gravel R.A.;
RT "Sequence homology around the biotin-binding site of human propionyl-
RT CoA carboxylase and pyruvate carboxylase.";
RL Arch. Biochem. Biophys. 254:631-636(1987).
RN [6]
RP SEQUENCE OF 1135-1178 FROM N.A.
RX MEDLINE=85030380; PubMed=6548474;
RA Freytag S.O., Collier K.J.;
RT "Molecular cloning of a cDNA for human pyruvate carboxylase.
RT Structural relationship to other biotin-containing carboxylases and
RT regulation of mRNA content in differentiating preadipocytes.";
RL J. Biol. Chem. 259:12831-12837(1984).
RN [7]
RP VARIANTS PC DEFICIENCY THR-610 AND ILE-743.
RX MEDLINE=98254451; PubMed=9585612;
RA Carbone M.A., MacKay N., Ling M., Cole D.E.C., Douglas C., Rigat B.,
RA Feigenbaum A., Clarke J.T.R., Haworth J.C., Greenberg C.R.,
RA Seargeant L., Robinson B.H.;
RT "Amerindian pyruvate carboxylase deficiency is associated with two
RT distinct missense mutations.";
RL Am. J. Hum. Genet. 62:1312-1319(1998).
RN [8]
RP VARIANTS PC DEFICIENCY ALA-145 AND CYS-451.

RX MEDLINE=98244401; PubMed=9585002;
RA Wexler I.D., Kerr D.S., Du Y., Kaung M.M., Stephenson W., Lusk M.M.,
RA Wappner R.S., Higgins J.J.;
RT "Molecular characterization of pyruvate carboxylase deficiency in two
RT consanguineous families."
RL Pediatr. Res. 43:579-584(1998).
CC -!- FUNCTION: Pyruvate carboxylase catalyzes a 2-step reaction,
CC involving the ATP-dependent carboxylation of the covalently
CC attached biotin in the first step and the transfer of the
CC carboxyl group to pyruvate in the second. Catalyzes in a tissue
CC specific manner, the initial reactions of glucose (liver, kidney)
CC and lipid (adipose tissue, liver, brain) synthesis from pyruvate.
CC -!- CATALYTIC ACTIVITY: ATP + pyruvate + HCO(3)(-) = ADP + phosphate +
CC oxaloacetate.
CC -!- COFACTOR: Biotin and manganese.
CC -!- PATHWAY: Gluconeogenesis and lipogenesis.
CC -!- SUBUNIT: Homotetramer.
CC -!- SUBCELLULAR LOCATION: Mitochondrial matrix.
CC -!- DISEASE: Defects in PC are the cause of pyruvate carboxylase
CC deficiency (PC deficiency) [MIM:266150]. PC deficiency leads to
CC lactic acidosis, mental retardation and death. It occurs in three
CC forms: mild or type A, severe neonatal or type B, and a very mild
CC lactic acidemia.
CC -!- SIMILARITY: WITH OTHER BIOTIN CARBOXYLASES, LIPOAMIDE TRANSFERASES
CC AND CARBAMYL PHOSPHATE SYNTHETASES.
CC
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CC -----
CC EMBL; U04641; AAA99537.1; -
CC EMBL; S72370; AAB31500.1; -
CC EMBL; U30891; AAA82937.1; -
CC EMBL; BC011617; AAH11617.1; -
CC EMBL; M26122; AAA36423.1; -
CC EMBL; K02282; AAA60033.1; -
CC PIR; G01933; JC2460.
CC HSSP; P24182; 1BNC.
CC Genew; HGNC:8636; PC.
CC GK; P11498; -
CC MIM; 266150; -
CC GO; GO:0005524; F:ATP binding; TAS.
CC GO; GO:0009374; F:biotin binding; TAS.
CC GO; GO:0004736; F:pyruvate carboxylase activity; TAS.
CC InterPro; IPR001882; Biotin_BS.
CC InterPro; IPR005482; Biotin_carb_C.
CC InterPro; IPR000089; Biotin_lipoyl.
CC InterPro; IPR005479; CPase_L_D2.
CC InterPro; IPR005481; CPase_L_N.
CC InterPro; IPR000891; HMGL-like.
CC InterPro; IPR003379; PYC_OADA.
CC InterPro; IPR005930; Pyruv_carbox.
CC Pfam; PF02785; Biotin_carb_C; 1.
CC Pfam; PF00364; biotin_lipoyl; 1.
CC Pfam; PF00289; CPase_L_chain; 1.
CC Pfam; PF02786; CPase_L_D2; 1.
CC Pfam; PF00682; HMGL-like; 1.
CC Pfam; PF02436; PYC_OADA; 1.
CC TIGRfams; TIGR01235; pyruv_carbox; 1.
CC PROSITE; PS00188; BIOTIN; 1.
CC Ligase; Multifunctional enzyme; Biotin; Manganese; Gluconeogenesis;
KW ATP-binding; Mitochondrion; lipid synthesis; Transit peptide;
KW Disease mutation.
KW TRANSIT 1 20 MITOCHONDRION (POTENTIAL).
FT CHAIN 21 1178 PYRUVATE CARBOXYLASE.
FT DOMAIN 21 549 BIOTIN CARBOXYLASE (BY SIMILARITY).
FT DOMAIN 550 1000 CARBOXYLTRANSFERASE (BY SIMILARITY).
FT DOMAIN 1096 1178 BIOTIN CARBOXYL CARRIER PROTEIN
FT (BY SIMILARITY).

NP BIND 198 203
ACT_SITE 328 328
BINDING 1144 1144
VARIANT 145 145
VARIANT 451 451
VARIANT 610 610
VARIANT 743 743
CONFLICT 225 226
CONFLICT 352 352
CONFLICT 385 386
CONFLICT 486 487
CONFLICT 638 638
CONFLICT 729 729
CONFLICT 774 775
SEQUENCE 1178 AA; 129633 MW; 381F527553A20095 CRC64;
Query Match 19.7%; Score 121; DB 1; Length 1178;
Best Local Similarity 40.6%; Pred. No. 0.072; Indels 0; Gaps 0;
Matches 28; Conservative 13; Mismatches 28;
QY 53 EGEIPAPLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVLKRDV 112
Db 1109 KGQIGAPMPGKVIDIKVVAGAKVAKGQPLCVLSAMKMETVVTSPMEGTVRKVHVTKDRTL 1168
QY 113 QGGQGLIKI 121
Db 1169 EGGDLILEI 1177
RESULT 28
PYC_RAT PYC_RAT STANDARD; PRT; 1178 AA.
ID PYC_RAT
AC P52873; Q64555;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Pyruvate carboxylase, mitochondrial precursor (EC 6.4.1.1) (Pyruvic
DE carboxylase) (PCB).
GN PC.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=96096548; PubMed=8522203;
RA Lehn D.A., Moran S.M., Macdonald M.J.;
RT "The sequence of the rat pyruvate carboxylase-encoding cDNA.";
RL Gene 165:331-332(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Wistar; TISSUE=Liver;
RX MEDLINE=96257760; PubMed=8687410;
RA Jitrapakdee S., Booker G.W., Cassady A.I., Wallace J.C.;
RT "Cloning, sequencing and expression of rat liver pyruvate
RT carboxylase.";
RL Biochem. J. 316:631-637(1996).
CC -!- FUNCTION: Pyruvate carboxylase catalyzes a 2-step reaction,
CC involving the ATP-dependent carboxylation of the covalently
CC attached biotin in the first step and the transfer of the carboxyl
CC group to pyruvate in the second. Catalyzes in a tissue specific
CC manner, the initial reactions of glucose (liver, kidney) and lipid
CC (adipose tissue, liver, brain) synthesis from pyruvate.
CC -!- CATALYTIC ACTIVITY: ATP + pyruvate + HCO(3)(-) = ADP + phosphate +
CC oxaloacetate.
CC -!- COFACTOR: Biotin and manganese (By similarity).
CC -!- PATHWAY: Gluconeogenesis and lipogenesis.
CC -!- SUBUNIT: Homotetramer (By similarity).

Best Local Similarity 37.7%; Pred. No. 0.015; Matches 23; Conservative 13; Mismatches 25; Indels 0; Gaps 0;

QY 55 EIPAPLAGTVSKILVKEGDTVKGAGQTVLVLEAMKMETEINAPTQKVEKVLVKERDAVQG 114
Db 3 DVRAEIVASVLEVVVNEGQIDKGDVVVLLESMKMEIPVLABAAGTVSKVAVSVGVDVIOA 62

QY 115 G 115
Db 63 G 63

RESULT 33
BCCP SOYBN
ID BCCP SOYBN STANDARD; PRT; 262 AA.
AC Q42783;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Biotin carboxyl carrier protein of acetyl-CoA carboxylase, chloroplast precursor (BCCP).
GN ACCB-1.
OS Glycine max (Soybean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eusoids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
OX NCBI_TaxID=3847;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC STRAIN=cv. Resnik;
RA Reverdatto S.V., Beilinson V., Neilsen N.C.;
RT "Characterization of a cDNA clone encoding a BCCP subunit of acetyl-CoA carboxylase from soybean."
RL (In) Plant Gene Register PGR96-040.
CC -!- FUNCTION: This protein is a component of the acetyl coenzyme A carboxylase complex; first, biotin carboxylase catalyzes the carboxylation of the carrier protein and then the transcarboxylase transfers the carboxyl group to form malonyl-CoA.
CC -!- PATHWAY: Long-chain fatty acid biosynthesis; first step.
CC -!- SUBCELLULAR LOCATION: Chloroplast.
CC
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CC
CC EMBL; U40666; AAB67836.1; -.
CC PIR; T06600; T06600.
CC HSSP; P02905; 3BDO.
CC InterPro; IPR001249; AcCoA biotinCC.
CC InterPro; IPR001882; Biotin_BS.
CC InterPro; IPR000089; Biotin_lipoyl.
CC Pfam; PF00364; biotin lipoyl; 1.
CC PRINTS; PR01071; ACOABIOTINCC.
CC TIGRFAMS; TIGR00531; BCCP; 1.
CC PROSITE; PS00188; BIOTIN; 1.
KW Fatty acid biosynthesis; Biotin; Chloroplast; Transit peptide.
FT TRANSIT 1 47
FT CHAIN 48 262 BIOTIN CARBOXYL CARRIER PROTEIN OF ACETYL-COA CARBOXYLASE.
FT BINDING 227 227 BIOTIN (BY SIMILARITY).
FT SEQUENCE 262 AA; 27657 MW; 79B273BD8B87DF48 CRC64;
SQ
Query Match 18.7%; Score 115; DB 1; Length 262;
Best Local Similarity 25.0%; Pred. No. 0.051;
Matches 36; Conservative 24; Mismatches 46; Indels 38; Gaps 5;

QY 1 MKLKVTYNGTAYDVEDVDKSH-----ENPMGTILFGGTGGAP----- 39
Db 114 LKLLK-----QHDVEVTIRKKEAMPQPPAPQPSVSVSPPPALPPPPVAPTPTLAR 167

[1]
SEQUENCE FROM N.A.
SPECIES=M.tuberculosis; STRAIN=H37RV;
RX MEDLINE=98295987; PubMed=9634230;
RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D., Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaiia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S., Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
RT "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence."
RL Nature 393:537-544(1998).
[2]
SEQUENCE FROM N.A.
SPECIES=M.tuberculosis; STRAIN=CDC 1551 / Oshkosh;
RX MEDLINE=22206494; PubMed=12218036;
RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O., Peterson J., DeBoy R., Dodson R., Gwinn M., Haft D., Hickey E., S.L., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg S.L., Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A., Bishai W., Jacobs W.R. Jr., Venter J.C., Fraser C.M.;
RT "Whole-genome comparison of Mycobacterium tuberculosis clinical and laboratory strains."
RL J. Bacteriol. 184:5479-5490(2002).
[3]
SEQUENCE OF 1-15, AND BIOTINYLATION.
SPECIES=M.tuberculosis;
RX MEDLINE=20072687; PubMed=10603390;
RA Skjot R.L., Oettinger T., Rosenkrands I., Ravn P., Brock I., Jacobsen S., Andersen P.;
RT "Comparative evaluation of low-molecular-mass proteins from Mycobacterium tuberculosis identifies members of the ESAT-6 family as immunodominant T-cell antigens."
RL Infect. Immun. 68:214-220(2000).
[4]
SEQUENCE FROM N.A.
SPECIES=M.bovis; STRAIN=AF2122/97;
RX MEDLINE=22709107; PubMed=12788972;
RA Garnier T., Eiglmeier K., Camus J.-C., Medina N., Mansoor H., Pryor M., Duthoy S., Grondin S., Lacroix C., Monsempe C., Simon S., Harris B., Atkin R., Doggett J., Mayes R., Keating L., Wheeler P.R., Parkhill J., Barrell B.G., Cole S.T., Gordon S.V., Hewinson R.G.;
RT "The complete genome sequence of Mycobacterium bovis."
RL Proc. Natl. Acad. Sci. U.S.A. 100:7877-7882(2003).
CC
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CC
CC EMBL; Z95120; CAB08316.1; -.
CC EMBL; AE007143; AAK47659.1; ALT INIT.
CC EMBL; BX248345; CAD95339.1; -.
CC PIR; F70596; F70596.
CC HSSP; P10802; 1IYU.
CC TIGR; MT3317; -.
CC TuberculList; RV3221C; -.
CC InterPro; IPR001882; Biotin_BS.
CC InterPro; IPR000089; Biotin_lipoyl.
CC Pfam; PF00364; biotin lipoyl; 1.
CC PROSITE; PS00188; BIOTIN; FALSE_NEG.
KW Biotin; Antigen; Complete proteome.
FT INIT MET 0
FT BINDING 36 36 BIOTIN (BY SIMILARITY).
FT SEQUENCE 70 AA; 7175 MW; 08B82DDD3A76892D CRC64;
SQ
Query Match 18.7%; Score 115; DB 1; Length 70;

Db 16 GTVAEVLVKVGVVKEGQSLYFVETDKVNSEIPAPVAGKIIVINIKAGQEIKVGVVMEI 75

RESULT 35

BCCP_HAEIN
ID BCCP_HAEIN STANDARD; PRT; 155 AA.
AC P43874;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Biotin carboxyl carrier protein of acetyl-CoA carboxylase (BCCP).
GN ACCB OR FASE OR HI0971.
OS Haemophilus influenzae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Haemophilus.
OX NCBI_TaxID=727;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Rd / KW20 / ATCC 51907;
RX MEDLINE=95350630; PubMed=7542800;
RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
RA Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
RA McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
RA Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
RA Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
RA Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
RA Venter J.C.;
RT "Whole-genome random sequencing and assembly of Haemophilus influenzae
Rd.";
RL Science 269:496-512(1995).
RN [2]
RP SEQUENCE OF 1-10.
RX MEDLINE=20137488; PubMed=10675023;
RA Langen H., Takacs B., Evers S., Berndt P., Lahm H.W., Wipf B.,
RA Gray C., Fountoulakis M.;
RT "Two-dimensional map of the proteome of Haemophilus influenzae.";
RL Electrophoresis 21:411-429(2000).
CC -!- FUNCTION: This protein is a component of the acetyl coenzyme A
CC carboxylase complex; first, biotin carboxylase catalyzes the
CC carboxylation of the carrier protein and then the transcarboxylase
CC transfers the carboxyl group to form malonyl-CoA (By similarity).
CC -!- PATHWAY: Long-chain fatty acid biosynthesis; first step.
CC -!- SUBUNIT: Homodimer (By similarity).

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or send an email to license@isb-sib.ch).

EMBL; U32778; AAC22631.1; -;
DR PIR; E64105; E64105.
DR HSSP; P02905; 1BDO.
DR TIGR; HI0971; -;
DR InterPro; IPR001249; ACcoA_biotinCC.
DR InterPro; IPR001882; Biotin_BS.
DR InterPro; IPR000089; Biotin_lipoyl.
DR Pfam; PF00364; biotin_lipoyl; 1.
DR PRINTS; PR01071; ACOAB10TINCC.
DR TIGRFAMs; TIGR00531; BCCP; 1.
DR PROSITE; PS00188; BIOTIN; 1.
DR Fatty acid biosynthesis; Biotin; Complete proteome.
KW BINDING 121 121 BIOTIN (BY SIMILARITY).
FT SEQUENCE 155 AA; 16247 MW; 696F19B4429A03CD CRC64;
SQ

Query Match 18.2%; Score 112; DB 1; Length 155;
Best Local Similarity 31.2%; Pred. No. 0.053;
Matches 30; Conservative 16; Mismatches 38; Indels 12; Gaps 2;

QY 40 -APAGAGAGAGAGEIP---APLAGTVSK-----ILVKEGDTVKGQTVLVLEAMK 88
Db 168 ATPTPTSPAPVAKSAKSLPPLKSEMGATFYRSPAPGEPFVKVGVGDKVKKGVVCIIEAMK 227

QY 89 METEINAPTDGKVEKVLVKERDAV 112

Db 228 LMNEIEADQSGTIVEIVAEDAKSV 251

RESULT 34

ODP2_MYCCA
ID ODP2_MYCCA STANDARD; PRT; 438 AA.
AC Q49110;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Dihydrolipoamide acetyltransferase component of pyruvate dehydrogenase
DE complex (EC 2.3.1.12) (E2).
GN PDHC OR ODP2.
OS Mycoplasma capricolum.
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
OX NCBI_TaxID=2095;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97001869; PubMed=8844861;
RA Zhu P.P., Peterkofsky A.;
RT "Sequence and organization of genes encoding enzymes involved in
pyruvate metabolism in Mycoplasma capricolum.";
RL Protein Sci. 5:1719-1736(1996).
CC -!- FUNCTION: THE PYRUVATE DEHYDROGENASE COMPLEX CATALYZES THE OVERALL
CC CONVERSION OF PYRUVATE TO ACETYL-COA & CO(2). IT CONTAINS MULTIPLE
CC COPIES OF THREE ENZYMOLOGICAL COMPONENTS: PYRUVATE DEHYDROGENASE (E1),
CC DIHYDROLIPOAMIDE ACETYLTRANSFERASE (E2) & LIPOAMIDE DEHYDROGENASE
CC (E3) (BY SIMILARITY).
CC -!- CATALYTIC ACTIVITY: Acetyl-CoA + dihydrolipoamide = CoA + S-
CC acetyldihydrolipoamide.
CC -!- COFACTOR: Contains 1 covalently bound lipoyl cofactor (By
CC similarity).
CC -!- SUBUNIT: Forms a 24-polypeptide structural core with octahedral
CC symmetry (By similarity).
CC -!- SIMILARITY: Belongs to the 2-oxoacid dehydrogenase family.
CC -!- SIMILARITY: Contains 1 lipoyl-binding domain.

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EMBL; U62057; AAC44344.1; -;
DR HSSP; P07016; 1C4T.
DR InterPro; IPR001078; 2Oxoacid_dh.
DR InterPro; IPR000089; Biotin_lipoyl.
DR InterPro; IPR004167; E3_binding.
DR InterPro; IPR003016; Lipoyl_BS.
DR Pfam; PF00198; 2-oxoacid_dh; 1.
DR Pfam; PF00364; biotin_lipoyl; 1.
DR Pfam; PF02817; e3_binding; 1.
DR ProDom; PD001115; 2Oxoacid_dh; 1.
DR PROSITE; PS00189; LIPOYL; 1.
KW Glycolysis; Transferase; Acyltransferase; Lipoyl.
FT BINDING 42 42 LIPOYL (BY SIMILARITY).
FT ACT SITE 411 411 POTENTIAL.
FT SEQUENCE 438 AA; 46927 MW; 4BF83B697480B4AB CRC64;
SQ

Query Match 18.5%; Score 114; DB 1; Length 438;
Best Local Similarity 38.3%; Pred. No. 0.097;
Matches 23; Conservative 16; Mismatches 21; Indels 0; Gaps 0;

QY 62 GTVSKILVKEGDTVKGQTVLVLEAMKMETEINAPTDGKVEKVLVKERDAVQGGGLIKI 121


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DR EMBL; AP002545; BAA98393.1; --
DR EMBL; AE017157; AAP98119.1; --
DR PIR; F72110; F72110.
DR PIR; G86513; G86513.
DR HSSP; P02905; 3BDO.
DR PHCI-2DPAGE; Q9Z901; --
DR TIGR; CP0585; --
DR InterPro; IPR001249; AcCoA_biotinCC.
DR InterPro; IPR001882; Biotin_BS.
DR InterPro; IPR000089; Biotin_lipoyl.
DR Pfam; PF00364; biotin_lipoyl; 1.
DR PRINTS; PR01071; ACOABIOTINCC.
DR TIGRFAMS; TIGR00531; BCCP; 1.
DR PROSITE; PS00188; BIOTIN; 1.
KW Fatty acid biosynthesis; Biotin; Complete proteome.
FT BINDING 129 129 BIOTIN (BY SIMILARITY).
SQ SEQUENCE 167 AA; 18461 MW; AAA1CF1801F9CE4C CRC64;

Query Match 17.6%; Score 108.5; DB 1; Length 167;
Best Local Similarity 38.4%; Pred. No. 0.1;
Matches 28; Conservative 9; Mismatches 29; Indels 7; Gaps 1;

QY 56 IPAPLAGTV-----SKILVKEGDTVKAGQTVLVLEAMKMETEINAPTQKVEKVLVKE 108
Db |::||| |::||| |::||| |::||| |::||| |::||| |::||| |::|||
QY 109 RDAVQGGGLIKI 121
Db |::||| |::||| |::||| |::||| |::||| |::||| |::||| |::|||
QY 150 GDPVQFGSKLFRI 162
Db |::||| |::||| |::||| |::||| |::||| |::||| |::||| |::|||

RESULT 38
ODO2_MYCTU STANDARD; PRT; 553 AA.
AC Q10381;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Dihydrolipoamide succinyltransferase component of 2-oxoglutarate
DE dehydrogenase complex (EC 2.3.1.61) (E2).
GN SUCB OR RV2215 OR MT2272 OR MTCY190.26 OR MB2238.
OS Mycobacterium tuberculosis, and
OS Mycobacterium bovis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1773, 1765;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=M.tuberculosis; STRAIN=H37Rv;
RX MEDLINE=98295987; PubMed=9634230;
RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
RA Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekala F.,
RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
RA Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
RA Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
RT "Deciphering the biology of Mycobacterium tuberculosis from the
complete genome sequence."
RL Nature 393:537-544 (1998).
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=M.tuberculosis; STRAIN=CDC 1551 / Oshkosh;
RX MEDLINE=2206494; PubMed=12218036;
RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
RA Peterson J., DeBoy R., Dodson R., Gwinn M., Haft D., Hickey E.,
RA Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg S.L.,
RA Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
RA Bishai W., Jacobs W.R. Jr., Venter J.C., Fraser C.M.;
RT "Whole-genome comparison of Mycobacterium tuberculosis clinical and
laboratory strains."
RL J. Bacteriol. 184:5479-5490 (2002).
```

```
RN [3]
RP SEQUENCE FROM N.A.
RC SPECIES=M.bovis; STRAIN=AF2122/97;
RX MEDLINE=22709107; PubMed=12788972;
RA Garnier T., Eiglmeier K., Camus J.-C., Medina N., Mansoor H.,
RA Pryor M., Duthoy S., Grondin S., Lacroix C., Monsempe C., Simon S.,
RA Harris B., Atkin R., Doggett J., Mayes R., Keating L., Wheeler P.R.,
RA Parkhill J., Barrell B.G., Cole S.T., Gordon S.V., Hewinson R.G.;
RT "The complete genome sequence of Mycobacterium bovis."
Proc. Natl. Acad. Sci. U.S.A. 100:7877-7882 (2003).
CC -!- FUNCTION: THE 2-OXOGLUTARATE DEHYDROGENASE COMPLEX CATALYZES THE
OVERALL CONVERSION OF 2-OXOGLUTARATE TO SUCCINYL-COA & CO(2). IT
CONTAINS MULTIPLE COPIES OF 3 ENZYMIC COMPONENTS: 2-OXOGLUTARATE
DEHYDROGENASE (E1), DIHYDROLIPOAMIDE SUCCINYLTRANSFERASE (E2) AND
LIPOAMIDE DEHYDROGENASE (E3) (BY SIMILARITY).
CC -!- CATALYTIC ACTIVITY: Succinyl-CoA + dihydrolipoamide = CoA + S-
succinylidihydrolipoamide.
CC -!- COFACTOR: Contains 2 covalently bound lipoyl cofactors
(Potential).
CC -!- PATHWAY: Tricarboxylic acid cycle.
CC -!- SUBUNIT: Forms a 24-polypeptide structural core with octahedral
symmetry (By similarity).
CC -!- SIMILARITY: Belongs to the 2-oxoacid dehydrogenase family.
CC -!- SIMILARITY: Contains 2 lipoyl-binding domains.
CC -----
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CC -----
DR EMBL; Z70283; CAA94256.1; --
DR EMBL; AE007072; AAK46557.1; --
DR EMBL; BX248341; CAD97091.1; --
DR PIR; H70786; H70786.
DR HSSP; P07016; 1C4T.
DR TIGR; MT2272; --
DR TuberculList; RV2215; --
DR InterPro; IPR001078; 2Oxoacid dh.
DR InterPro; IPR000089; Biotin_lipoyl.
DR InterPro; IPR004167; E3_binding.
DR InterPro; IPR003016; Lipoyl_BS.
DR Pfam; PF00198; 2-oxoacid dh; 1.
DR Pfam; PF00364; biotin_lipoyl; 2.
DR Pfam; PF02817; e3_binding; 1.
DR ProDom; PD001115; 2Oxoacid dh; 1.
DR PROSITE; PS00189; LIPOYL; 2.
KW Tricarboxylic acid cycle; Transferase; Acyltransferase; Lipoyl;
KW Complete proteome.
FT BINDING 43 43 LIPOYL (POTENTIAL).
FT BINDING 162 162 LIPOYL (POTENTIAL).
FT ACT_SITE 523 523 BY SIMILARITY.
FT ACT_SITE 527 527 BY SIMILARITY.
SQ SEQUENCE 553 AA; 57087 MW; 54B6E70D23B804A7 CRC64;

Query Match 17.6%; Score 108; DB 1; Length 553;
Best Local Similarity 37.7%; Pred. No. 0.34;
Matches 23; Conservative 16; Mismatches 22; Indels 0; Gaps 0;

QY 62 GTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTQKVEKVLVKEKVGGLIKI 121
Db |::||| |::||| |::||| |::||| |::||| |::||| |::||| |::|||
QY 122 G 122
Db 77 G 77

RESULT 39
BTB7_MYCLE STANDARD; PRT; 70 AA.
ID BTB7_MYCLE
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AC Q9CCH9;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Biotinylated protein TB7.3 homolog.
GN ML0802.
OS Mycobacterium leprae.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1769;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=TN;
RX MEDLINE=21128732; PubMed=11234002;
RA Cole S.T., Eiglmeier K., Parkhill J., James K.D., Thomson N.R.,
RA Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D.,
RA Mungall K., Basham D., Brown D., Chillingworth T., Connor R.,
RA Davies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N.,
RA Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S.,
RA Murphy L., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M.,
RA Rutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R.,
RA Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R.,
RA Barrell B.G.;
RT "Massive gene decay in the leprosy bacillus.";
RL Nature 409:1007-1011(2001).
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AL583919; CAC30312.1; ALT_INIT.
DR HSSP; P10802; 11YU.
DR Leproma; ML0802; -;
DR InterPro; IPR001882; Biotin BS.
DR InterPro; IPR000089; Biotin_lipoyl.
DR Pfam; PF00364; biotin_lipoyl; 1.
DR PROSITE; PS00188; BIOTIN; FALSE_NEG.
KW Biotin; Complete proteome.
FT INIT MET 0 0 BY SIMILARITY.
FT BINDING 36 36 BIOTIN (BY SIMILARITY).
SQ SEQUENCE 70 AA; 7088 MW; B519F389DEF0447D CRC64;

Query Match 17.4%; Score 107; DB 1; Length 70;
Best Local Similarity 36.1%; Pred. No. 0.06;
Matches 22; Conservative 14; Mismatches 25; Indels 0; Gaps 0;

QY 55 EIPAPLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTQKVKVVKERDAVQG 114
Db 3 DVRAEIVASVLEVTVSEGDQIGKGDVLVLESKMKEIPVLGAGIVSKVSVSGDVIIQA 62

QY 115 G 115
Db 63 G 63

RESULT 40
ODP2_HAEIN STANDARD; PRT; 567 AA.
AC P45118;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Dihydrolipoamide acetyltransferase component of pyruvate dehydrogenase
DE complex (EC 2.3.1.12) (E2).
GN ACEF OR H11232.
OS Haemophilus influenzae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Haemophilus.
OX NCBI_TaxID=727;

RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=rd / KW20 / ATCC 51907;
RX MEDLINE=95350630; PubMed=7542800;
RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
RA Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
RA McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
RA Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
RA Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
RA Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
RA Venter J.C.;
RT "Whole-genome random sequencing and assembly of Haemophilus influenzae
Rd.";
RL Science 269:496-512(1995).
CC -!- FUNCTION: THE PYRUVATE DEHYDROGENASE COMPLEX CATALYZES THE OVERALL
CC CONVERSION OF PYRUVATE TO ACETYL-COA & CO(2). IT CONTAINS MULTIPLE
CC COPIES OF THREE ENZYMIC COMPONENTS: PYRUVATE DEHYDROGENASE (E1),
CC DIHYDROLIPOAMIDE ACETYLTRANSFERASE (E2) & LIPOAMIDE DEHYDROGENASE
CC (E3) (BY SIMILARITY).
CC -!- CATALYTIC ACTIVITY: Acetyl-CoA + dihydrolipoamide = CoA + S-
CC acetyldihydrolipoamide.
CC -!- COFACTOR: Contains 2 covalently bound lipoyl cofactors (By
CC similarity).
CC -!- SUBUNIT: Forms a 24-polypeptide structural core with octahedral
CC symmetry (By similarity).
CC -!- SIMILARITY: Belongs to the 2-oxoacid dehydrogenase family.
CC -!- SIMILARITY: Contains 2 lipoyl-binding domains.
CC -----
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CC -----
DR EMBL; U32803; AAC22885.1; -;
DR PIR; I64111; I64111.
DR HSSP; P10802; 1DPC.
DR TIGR; H11232; -;
DR InterPro; IPR001078; 2Oxoacid_dh.
DR InterPro; IPR006256; AceF.
DR InterPro; IPR000089; Biotin_lipoyl.
DR InterPro; IPR004167; E3_binding.
DR InterPro; IPR003016; Lipoyl_BS.
DR Pfam; PF00198; 2-oxoacid_dh; 1.
DR Pfam; PF00364; biotin_lipoyl; 2.
DR Pfam; PF02817; e3_binding; 1.
DR ProDom; PD001115; 2Oxoacid_dh; 1.
DR TIGRFAMs; TIGR01348; PDHac_trf_long; 1.
DR PROSITE; PS00189; LIPOYL; 2.
KW Glycolysis; Transferase; Acyltransferase; Repeat; Lipoyl;
KW Complete proteome.
FT DOMAIN 1 245 LIPOYL BINDING, ACIDIC.
FT DOMAIN 247 567 SUBUNIT BINDING, CATALYTIC.
FT BINDING 41 41 LIPOYL (BY SIMILARITY).
FT BINDING 147 147 LIPOYL (BY SIMILARITY).
FT ACT_SITE 484 484 POTENTIAL.
FT ACT_SITE 540 540 POTENTIAL.
FT ACT_SITE 544 544 POTENTIAL.
SQ SEQUENCE 567 AA; 59410 MW; 891DBCDEB388C5B0 CRC64;

Query Match 17.2%; Score 105.5; DB 1; Length 567;
Best Local Similarity 28.7%; Pred. No. 0.53;
Matches 39; Conservative 21; Mismatches 60; Indels 16; Gaps 4;

QY 1 MKLKVTVNGTAYDQVDV-DK-SHENPMGTILFGGGTGGAPAPAGAGAGKA----- 51
Db 44 MEVPAPEAGVVKEILVKGDKVSTGTPTMLVLEAAGAAPAADEPTAPVATAPVATAP 103
QY 52 ---GEGEIPAPLAG-----TVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTQKVKV 104

Db 104 TASAIVEVNVDPDIGGDEVNVTIIMVAVGDTITTEEQSLITVEGDKASMEVPAPFGGVVKEI 163
QY 105 LVKERDAVQGGQGLIK 120
Db 164 LVKSGDKVSTGSLIMR 179

Search completed: March 3, 2004, 10:29:43
Job time : 13.7083 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 3, 2004, 10:26:14 ; Search time 10.2083 Seconds
(without alignments)
659.599 Million cell updates/sec

Title: US-09-987-485A-2
Perfect score: 342
Sequence: 1 EGEIPAPLAGTVSKILVKEG.....KVLVKERDAVQGQGLIKIG 70

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_78:*
1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	342	100.0	123	1 BKIP	biotin carboxyl ca
2	195	57.0	145	2 F75135	methylmalonyl-coa
3	189	55.3	149	2 A71074	probable methylmal
4	180	52.6	571	2 F71133	probable oxaloacet
5	178	52.0	140	2 H69526	methylmalonyl-CoA
6	174	50.9	655	2 B70432	pyruvate carboxyla
7	174	50.9	984	2 T44608	pyruvate carboxyla
8	173	50.6	567	2 F64453	oxaloacetate decar
9	170	49.7	186	2 D90418	hypothetical prote
10	167	48.8	134	2 C72341	propionyl-CoA carb
11	167	48.8	1144	2 D97227	pyruvate carboxyla
12	165	48.2	596	2 A28088	oxaloacetate decar
13	164	48.0	597	2 G82308	oxaloacetate decar
14	163	47.7	599	2 D81367	probable pyruvate
15	161	47.1	142	2 D69510	oxaloacetate decar
16	159.5	46.6	576	2 AC3038	biotin carboxylase
17	159.5	46.6	576	2 H98247	biotin carboxylase
18	159	46.5	665	2 G97819	hypothetical prote
19	158	46.2	607	2 F82966	probable transcarb
20	157	45.9	1146	2 AC1565	pyruvate carboxyla
21	157	45.9	1146	2 AH1208	pyruvate carboxyla
22	157	45.9	1150	2 A83978	pyruvate carboxyla
23	153	44.7	620	2 F70439	oxaloacetate decar
24	152	44.4	167	2 T44291	biotin carboxyl ca
25	152	44.4	436	2 A53568	methylcrotonoyl-Co
26	152	44.4	591	2 B44465	sodium ion pump ox
27	150	43.9	70	2 E83791	hypothetical prote
28	150	43.9	665	2 C71667	propionyl-CoA carb
29	148	43.3	591	2 AB0509	oxaloacetate decar

30	148	43.3	591	2 AE0909	oxaloacetate decar
31	148	43.3	1174	2 AE2911	pyruvate carboxyla
32	148	43.3	1174	2 C97686	pyruvate carboxyla
33	146	42.7	1150	2 G89881	pyruvate carboxyla
34	145	42.4	655	2 A83395	probable acyl-CoA
35	144	42.1	161	2 A95049	hypothetical prote
36	144	42.1	161	2 G97919	acetyl-CoA carboxy
37	143	41.8	730	2 G86161	hypothetical prote
38	143	41.8	1137	2 E86708	pyruvate carboxyla
39	143	41.8	1185	2 T39734	pyruvate carboxyla
40	142	41.5	155	2 H86721	hypothetical prote
41	141	41.2	1078	2 D87647	hypothetical prote
42	140	40.9	568	2 C69014	oxaloacetate decar
43	139.5	40.8	1127	2 D70671	pyruvate carboxyla
44	138.5	40.5	157	2 S73204	acetyl-CoA carboxy
45	138	40.4	129	2 D49094	methylmalonyl-CoA

ALIGNMENTS

RESULT 1

BKIP

biotin carboxyl carrier protein [validated] - Propionibacterium freudenreichii subsp. s.
N:Alternate names: methylmalonyl-CoA carboxyltransferase biotin carboxyl carrier protein
C:Species: Propionibacterium freudenreichii subsp. shermanii
C:Date: 31-Mar-1980 #sequence_revision 31-Mar-1980 #text_change 01-Feb-2002
C:Accession: A03401

R;Maloy, W.L.; Bowlen, B.U.; Zwolinski, G.K.; Kumar, K.G.; Wood, H.G.; Ericsson, L.H.;
J. Biol. Chem. 254, 11615-11622, 1979

A;Title: Amino acid sequence of the biotinyl subunit from transcarboxylase.

A;Reference number: A03401; MUID:80049796; PMID:40985

A;Accession: A03401

A;Molecule type: protein

A;Residues: 1-123 <MAL>

C;Comment: Six or 12 chains of biotin carboxyl carrier protein (BCCP) are found in the
onyl coenzyme A to BCCP and (2) from BCCP to pyruvate, forming oxalacetate.

C;Comment: See PIR:A48665 and PIR:S36808.

C;Superfamily: biotin carboxyl carrier protein; lipoyl/biotin-binding homology

C;Keywords: biotin binding

F;50-123/Domain: lipoyl/biotin-binding homology <LPB>

F;89/Binding site: biotin (Lys) (covalent) #status experimental

Query Match 100.0%; Score 342; DB 1; Length 123;
Best Local Similarity 100.0%; Pred.No. 2.1e-27;
Matches 70; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGEIPAPLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVLVKERDAV 60

Db 54 EGEIPAPLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVLVKERDAV 113

Qy 61 QGGQGLIKIG 70

Db 114 QGGQGLIKIG 123

RESULT 2

F75135

methylmalonyl-coa decarboxylase gamma chain PAB1771 - Pyrococcus abyssi (strain Orsay)

C;Species: Pyrococcus abyssi

C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000

C;Accession: F75135

R;anonymous, Genoscope

submitted to the EMBL Data Library, July 1999

A;Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome str

A;Reference number: A75001

A;Accession: F75135

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-145 <KAW>

A;Cross-references: GB:AJ248285; GB:AL096836; NID:G5458067; PIDN:CAB49799.1; PID:G54583:

A;Experimental source: strain Orsay

C;Genetics:


```

.: Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: F82966
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-607 <STO>
A;Cross-references: GB:AE004956; GB:AE004091; NID:g9951760; PIDN:AAG08820.1; GSPDB:GN001
A;Experimental source: strain PA01
C;Genetics:
C;Gene: PA5435
C;Superfamily: Klebsiella pneumoniae oxaloacetate decarboxylase alpha chain; lipoyl/biot
Query Match 46.2%; Score 158; DB 2; Length 607;
Best Local Similarity 48.5%; Pred. NO. 3.2e-08;
Matches 33; Conservative 12; Mismatches 23; Indels 0; Gaps 0;
QY 2 GEIPAPLAGTVSKIIIVKEGDTVKAGQTVLVLEAMKMETEINAPTGDGKVEKVLKERVAVQ 61
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 538 GHVSTTTPGNIVDLVKEGDSVKAGQAVLITEAMKMETETEVQAGIAGTVKAIHVAKGDRVN 597
QY 62 GGQGLIKI 69
| : : : : : : : : : : : : : : : : : : : : : :
Db 598 PGEILIEI 605

```

RESULT 20
AC1565
pyruvate carboxylase homolog pycA [imported] - *Listeria innocua* (strain Clip11262)
C/Species: *Listeria innocua*
C/Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 14-Dec-2001
C/Accession: AC1565
R/Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A/Authors: Kref, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
A./Title: Comparative genomics of *Listeria* species.
A/Reference number: AB1077; MUID:21537279; PMID:11679669
A/Accession: AC1565
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-1146 <GLA>
A/Cross-references: GB:AL592022; PIDN:CAC96291.1; PID:g16413519; GSPDB:GN00178
A/Experimental source: strain Clip11262
C/Genetics:
A/Gene: pycA
C/Superfamily: pyruvate carboxylase; biotin carboxylase homology; lipoyl/biotin-binding

RESULT 21
AH1208
pyruvate carboxylase homolog pycA [imported] - *Listeria monocytogenes* (strain EGD-e)
C/Species: *Listeria monocytogenes*
C/Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 14-Dec-2001
C/Accession: AH1208
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker
D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
D.; Jones, L.M.; Karst, U.

Science 294, 849-852, 2001
A;Authors: Krefit, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Mok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehlant, A.;Title: Comparative genomics of *Listeria* species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AH1208
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1146 <GLA>
A;Cross-references: GB:NC_003210; PIDN:CAC99150.1; PID:g16410474; GSPDB:GN00177
A;Experimental source: strain EGD-e

RESULT 22

A83978

pyruvate carboxylase pycA [imported] - Bacillus halodurans (strain C-125)

C/Species: Bacillus halodurans

C/Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001

C/Accession: A83978

R/Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hiraoka, Y.; Nishimura, K. 2000

Nucleic Acids Res. 28, 4317-4331, 2000

A/Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and its complete genome map

A/Reference number: A83650; MUID:20512582; PMID:11058132

A/Accession: A83978

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-1150 <STO>

A/Cross-references: GB:AP001516; GB:BA000004; NID:gl0175192; PIDN:BA06344.1; GSPDB:GN000001

A/Experimental source: strain C-125

C/Genetics:

A/Gene: pycA

C/Superfamily: pyruvate carboxylase; biotin carboxylase homology; lipoyl/biotin-binding site

RESULT 23
F70439
oxaloacetate decarboxylase alpha chain - Aquifex aeolicus
C;Species: Aquifex aeolicus
C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 18-Aug-2000
C;Accession: F70439
R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; C
V.
Nature 392, 353-358, 1998
A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A;Reference number: A70300; MUID:98196666; PMID:9537320
A;Accession: F70439

Db 59 AGSVFKILVAEGDTIEAGQVLLVLEAMKMETEITAPSAGVVGAINVKEGEAVQGGQSLIE 118
QY 121 I 121
Db 119 I 119

RESULT 2

Q9V0A6 PRELIMINARY; PRT; 145 AA.
AC Q9V0A6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Methylmalonyl-CoA decarboxylase gamma chain.
GN PYRAB08850 OR PAB1771.
OS Pyrococcus abyssi.
OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
OC Pyrococcus.
OX NCBI_TaxID=29292;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GES / Orsay;
RA Heilig R.;
RT "Pyrococcus abyssi genome sequence: insights into archaeal chromosome structure and evolution."
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ248285; CAB49799.1; --
DR PIR; F75135; F75135.
DR HSSP; P02905; 1BDO.
DR GO; GO:0009374; F:biotin binding; IEA.
DR InterPro; IPR001882; Biotin_BS.
DR InterPro; IPR000089; Biotin_lipoyl.
DR Pfam; PF00364; biotin_lipoyl; 1.
DR PROSITE; PS00188; BIOTIN; 1.
KW Complete proteome.
SQ SEQUENCE 145 AA; 15489 MW; 9C14433663F40D94 CRC64;

Query Match 37.6%; Score 231.5; DB 17; Length 145;

Best Local Similarity 41.4%; Pred. No. 1.8e-11;
Matches 60; Conservative 18; Mismatches 44; Indels 23; Gaps 3;
QY 1 MKLKVTVNGTAYDVVDV-----VDKSH-----NPMGTILFGGGTGAPA 40
Db 1 MKVKVVVNGKEYEVDVEEVPMPGKFRVTLGKTYEVEANLGIQVAPVQTQVATPAPTPT 60
QY 41 PA---AGGAGAGKAGEGEIPAPLAGTVSKILVKEGDTVKGQTVLVLEAMKMETEINAPT 97
Db 61 PTPVQAPPTTPQVQASENVVVTAPMPGKVLKILVQEGQQVKGQGLLILEAMKMETEINAPT 120
QY 98 DGKVEKVLVKERDAVQGGQGLIKIG 122
Db 121 DGVVVKRILVKEGDAVDGTGTLIELG 145

RESULT 3

O59021 PRELIMINARY; PRT; 149 AA.
AC O59021;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE 149AA long hypothetical methylmalonyl-CoA decarboxylase gamma chain.
GN PH1284.
OS Pyrococcus horikoshii.
OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
OC Pyrococcus.
OX NCBI_TaxID=53953;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=OT3;
RX MEDLINE=98344137; PubMed=9679194;

RA Kwarabayasi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y.,
RA Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y.,
RA Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y.,
RA Funahashi T., Tanaka T., Kudo H. Y., Yamazaki J., Kushida N., Oguchi A.,
RA Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,
RA Masuchi Y., Shizuya H., Kikuchi H.;
RT "Complete sequence and gene organization of the genome of a hyper-
RT thermophilic archaeobacterium, Pyrococcus horikoshii OT3.";
RL DNA Res. 5:55-76(1998).
DR EMBL; AP000005; BAA30387.1; --
DR PIR; A71074; A71074.
DR HSSP; P10802; 1IYU.
DR GO; GO:0009374; F:biotin binding; IEA.
DR InterPro; IPR001882; Biotin_BS.
DR InterPro; IPR000089; Biotin_lipoyl.
DR Pfam; PF00364; biotin_lipoyl; 1.
DR PROSITE; PS00188; BIOTIN; 1.
KW Complete proteome.
SQ SEQUENCE 149 AA; 15985 MW; 1C3AA5F47E6BA6F1 CRC64;

Query Match 35.9%; Score 221; DB 17; Length 149;

Best Local Similarity 36.3%; Pred. No. 1.3e-10;
Matches 53; Conservative 21; Mismatches 48; Indels 24; Gaps 1;
QY 1 MKLKVTVNGTAYDVVDV-----VDKSHENPMGTILFGGGTG 36
Db 4 MKVKVVVNGKEYEVEEVPMPGKFRVTLGKTYEVEVTSAGVTSKQVQVTPAPTAPA 63
QY 37 GAPAPAAAGGAGAGKAGEGEIPAPLAGTVSKILVKEGDTVKGQTVLVLEAMKMETEINAP 96
Db 64 PTPTPAPAPSSKTVVSENVVVSAPMPGKVLRLVVRGDRVVRVGQGLLVLEAMKMETEINAP 123
QY 97 TDGKVEKVLVKERDAVQGGQGLIKIG 122
Db 124 RDGVVVKRILVKEGEAVDTGQPLIELG 149

RESULT 4

Q8U303 PRELIMINARY; PRT; 144 AA.
AC Q8U303;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Methylmalonyl-CoA decarboxylase gamma chain.
GN PF0673.
OS Pyrococcus furiosus.
OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
OC Pyrococcus.
OX NCBI_TaxID=2261;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Vcl / DSM 3638 / ATCC 43587 / JCM 8422;
RA Weiss R.B., Dunn D.M., Robb F.T., Brown J.R.;
RT "The complete sequence of the Pyrococcus furiosus genome.";
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE010188; AAL80797.1; --
DR GO; GO:0009374; F:biotin binding; IEA.
DR InterPro; IPR001882; Biotin_BS.
DR InterPro; IPR000089; Biotin_lipoyl.
DR Pfam; PF00364; biotin_lipoyl; 1.
DR PROSITE; PS00188; BIOTIN; 1.
KW Complete proteome.
SQ SEQUENCE 144 AA; 15315 MW; 422C96A8ED809C6A CRC64;

Query Match 35.4%; Score 218; DB 17; Length 144;

Best Local Similarity 36.7%; Pred. No. 2.2e-10;
Matches 54; Conservative 21; Mismatches 44; Indels 28; Gaps 3;
QY 1 MKLKVTVNGTAYDVVDV-----VDKSHENPMGTILFGGGTGGA 38
Db 1 MKVKIVINGEYEVEEIMPGRFKVTLGKTYEVEAKDLGISTPAPVQV---PTPTPA 57

DR GO:0009374; F:biotin binding; IEA.
DR InterPro; IPR001882; Biotin_BS.
DR InterPro; IPR000089; Biotin_lipoyl.
DR Pfam; PF00364; biotin_lipoyl; 1.
DR PROSITE; PS00188; BIOTIN; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 116 AA; 12260 MW; FC4BC174CB6BAFFA CRC64;

Query Match 30.4%; Score 187; DB 16; Length 116;
Best Local Similarity 41.5%; Pred. No. 5.9e-08;
Matches 51; Conservative 11; Mismatches 45; Indels 16; Gaps 3;

QY 2 KLKVTVNGTAYDVVDVKSHENPMGTILFGGGTGGAPAPAAAGGA----GAGKAGEG-EI 56
Db 3 RYEVTVNGQVYEVS-----RELADGETVEVSQPAAPATEKEMNANAAGGGIQV 51

QY 57 PAPLAGTVSKILVKEGDTVKGQTVLVLEAMKMETEINAPTDGKVEKVLVKERDAVQGGQ 116
Db 52 KAPMSGTVLSIFATEGKAVKKGAEVLVLEAMKMWENEILAPADGLVSKIHVVANQTVSEQ 111

QY 117 GLI 119
Db 112 VLI 114

RESULT 13
Q8P104 PRELIMINARY; PRT; 116 AA.
AC Q8P104;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Putative methylmalonyl-CoA decarboxylase, gamma-subunit.
GN SPY18.1128.
OS Streptococcus pyogenes (serotype M18).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=186103;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=MGAS8232 / Serotype M18;
RX MEDLINE=21927593; PubMed=11917108;
RA Smoot J.C., Barbican K.D., Van Gompel J.J., Smoot L.M., Chaussee M.S.,
RA Sylva G.L., Sturdevant D.E., Ricklefs S.M., Porcella S.F.,
RA Parkins L.D., Beres S.B., Campbell D.S., Smith T.M., Zhang Q.,
RA Kapur V., Daly J.A., Veasy L.G., Musser J.M.;
RT "Genome sequence and comparative microarray analysis of serotype M18
RT group A Streptococcus strains associated with acute rheumatic fever
RT outbreaks.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:4668-4673 (2002).
DR EMBL; AE010038; AAL97749.1; -
DR GO:0009374; F:biotin binding; IEA.
DR InterPro; IPR001882; Biotin_BS.
DR InterPro; IPR000089; Biotin_lipoyl.
DR Pfam; PF00364; biotin_lipoyl; 1.
DR PROSITE; PS00188; BIOTIN; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 116 AA; 12290 MW; FC4BDE49CB6BAFFA CRC64;

Query Match 30.2%; Score 186; DB 16; Length 116;
Best Local Similarity 41.5%; Pred. No. 7.1e-08;
Matches 51; Conservative 11; Mismatches 45; Indels 16; Gaps 3;

QY 2 KLKVTVNGTAYDVVDVKSHENPMGTILFGGGTGGAPAPAAAGGA----GAGKAGEG-EI 56
Db 3 RYEVTVNGQVYEVS-----RELADGETVEVSQPAAPATEKEMNANAAGGGIQV 51

QY 57 PAPLAGTVSKILVKEGDTVKGQTVLVLEAMKMETEINAPTDGKVEKVLVKERDAVQGGQ 116
Db 52 KAPMSGTVLSIFATEGKAVKKGAEVLVLEAMKMWENEILAPADGLVSKIHVVANQTVSEQ 111

QY 117 GLI 119
Db 112 VLI 114

Db 112 VLI 114

RESULT 14
Q8A737 PRELIMINARY; PRT; 144 AA.
AC Q8A737;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Biotin carboxyl carrier protein (BCCP).
GN BT1688.
OS Bacteroides thetaiotaomicron.
OC Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
OC Bacteroidaceae; Bacteroides.
OX NCBI_TaxID=818;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=VPI-5482 / ATCC 29148;
RX MEDLINE=22550858; PubMed=12663928;
RA Xu J., Bjursell M.K., Himrod J., Deng S., Carmichael L.K.,
RA Chiang H.C., Hooper L.V., Gordon J.I.;
RT "A genomic view of the human-Bacteroides thetaiotaomicron symbiosis.";
RL Science 299:2074-2076(2003).
DR EMBL; AE016932; AAO76795.1; -
DR GO:0009317; C:acetyl-CoA carboxylase complex; IEA.
DR GO:0003989; F:acetyl-CoA carboxylase activity; IEA.
DR GO:0009374; F:biotin binding; IEA.
DR GO:0006633; P:fatty acid biosynthesis; IEA.
DR InterPro; IPR001249; AcCoA_biotinCC.
DR InterPro; IPR001882; Biotin_BS.
DR InterPro; IPR000089; Biotin_lipoyl.
DR Pfam; PF00364; biotin_lipoyl; 1.
DR PRINTS; PR01071; ACOABIOTINCC.
DR PROSITE; PS00188; BIOTIN; 1.
KW Complete proteome.
SQ SEQUENCE 144 AA; 15487 MW; 462383E2FB85601E CRC64;

Query Match 30.1%; Score 185; DB 16; Length 144;
Best Local Similarity 39.0%; Pred. No. 1.1e-07;
Matches 46; Conservative 18; Mismatches 52; Indels 2; Gaps 2;

QY 5 VTVNGTAYDVVDVDVD-KSHENPMGTILFGGGTGGAPAPAAAGGAGAGKAGEGEIPAPLAGT 63
Db 27 VEVNGTHYKVEMEKQPKTAPKV-VVRPMPNSPAAPTTPVVKPAAPSTGKSGVKSPLPGV 85

QY 64 VSKILVKEGDTVKGQTVLVLEAMKMETEINAPTDGKVEKVLVKERDAVQGGGLIKI 121
Db 86 ILDIKVNVDGTVKRGQTIILLEAMKMENNINADKGVTAINVNKGDSVLEGNLDVII 143

RESULT 15
Q9KUHI PRELIMINARY; PRT; 597 AA.
AC Q9KUHI;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Oxaloacetate decarboxylase, alpha subunit.
GN VC0550.
OS Vibrio cholerae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=666;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=E1 Tor N16961 / Serotype O1;
RX MEDLINE=20406833; PubMed=10952301;
RA Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
RA Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
RA Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
RA Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
RA McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,


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RA Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
RA Fraser C.M.;
RT "DNA sequence of both chromosomes of the cholera pathogen Vibrio
RT cholerae.";
RL Nature 406:477-483 (2000).
CC -1- COFACTOR: BIOTIN (BY SIMILARITY).
DR EMBL; AE004141; AAF93718.1; -.
DR PIR; G82308; G82308.
DR HSSP; P02905; 1BDO.
DR TIGR; VC0550; -.
DR GO; GO:0009374; F:biotin binding; IEA.
DR GO; GO:0003824; F:catalytic activity; IEA.
DR GO; GO:0008948; F:oxaloacetate decarboxylase activity; IEA.
DR GO; GO:0006814; P:sodium ion transport; IEA.
DR InterPro; IPR001882; Biotin_BS.
DR InterPro; IPR000089; Biotin_lipoyl.
DR InterPro; IPR000891; HMGL-like.
DR InterPro; IPR005776; Oada.
DR InterPro; IPR003379; PYC_OADA.
DR Pfam; PF00364; biotin_lipoyl; 1.
DR Pfam; PF00682; HMGL-like; 1.
DR Pfam; PF02436; PYC_OADA; 1.
DR TIGRFAMs; TIGR01108; oada; 1.
DR PROSITE; PS00188; BIOTIN; 1.
KW Biotin; Complete proteome.
SQ SEQUENCE 597 AA; 64795 MW; 033BF5F2209F5468 CRC64;

Query Match 30.1%; Score 185; DB 16; Length 597;
Best Local Similarity 39.3%; Pred. No. 5.7e-07;
Matches 46; Conservative 18; Mismatches 45; Indels 8; Gaps 2;

QY 5 VTVNGTAYDVDVDKSHENPMGTILFGGTTGGAPAPAGGAGKAGEGEIPAPLAGTV 64
Db 488 VKVDGVVVDVEV-----GSQQLTSVVPAGQKAAPKLA VATPTQGA EA-VAAPLAGTI 539

QY 65 SKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVLVKERDAVQGGGLIKI 121
Db 540 FKIQVEQGEVAEGDVLIVLEAMKMETEIRAARSGVIOELHVKEGDSVRVGASLLSL 596

RESULT 16
Q891Y8 PRELIMINARY; PRT; 986 AA.
AC Q891Y8;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Pyruvate carboxylase (EC 6.4.1.1).
GN CTC02224.
OS Clostridium tetani.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1513;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22457253; PubMed=12552129;
RA Brueggemann H., Baeumer S., Fricke W.F., Wierzer A., Liesegang H.,
RA Decker I., Herzberg C., Martinez-Arias R., Merkl R., Henne A.,
RA Gottschalk G.;
RT "The genome sequence of Clostridium tetani, the causative agent of
RT tetanus disease.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:1316-1321 (2003).
DR EMBL; AE015943; AAC36707.1; -.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0009374; F:biotin binding; IEA.
DR GO; GO:0016874; F:ligase activity; IEA.
DR GO; GO:0004736; F:pyruvate carboxylase activity; IEA.
DR InterPro; IPR001882; Biotin_BS.
DR InterPro; IPR005482; Biotin_carb_C.
DR InterPro; IPR000089; Biotin_lipoyl.
DR InterPro; IPR005479; CPase_L_D2.
DR InterPro; IPR000891; HMGL-like.
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DR InterPro; IPR003379; PYC_OADA.
DR Pfam; PF02785; Biotin_carb_C; 1.
DR Pfam; PF00364; biotin_lipoyl; 1.
DR Pfam; PF02786; CPSase_L_D2; 1.
DR Pfam; PF00682; HMGL-like; 1.
DR Pfam; PF02436; PYC_OADA; 1.
DR PROSITE; PS00188; BIOTIN; 1.
DR PROSITE; PS00867; CPSASE_2; 1.
KW Ligase; Complete proteome.
SQ SEQUENCE 986 AA; 110669 MW; 8825F618B0A4B219 CRC64;

Query Match 30.1%; Score 185; DB 16; Length 986;
Best Local Similarity 51.3%; Pred. No. 1e-06;
Matches 39; Conservative 13; Mismatches 24; Indels 0; Gaps 0;

QY 46 AGAGKAGEGEIPAPLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVL 105
Db 909 AMADKEDKSQIGASIPGNISKILIKEGDTVKNKGDRIAVIEAMKMETNIVSTVTGKVKIF 968

QY 106 VKERDAVQGGGLIKI 121
Db 969 VKENEQVKVGQLIIKI 984

RESULT 17
Q58564 PRELIMINARY; PRT; 571 AA.
AC Q58564;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE 571AA long hypothetical oxaloacetate decarboxylase alpha chain.
GN PH0834.
OS Pyrococcus horikoshii.
OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
OC Pyrococcus.
OX NCBI_TaxID=53953;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98344137; PubMed=9679194;
RA Kawarabayasi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y.,
RA Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y.,
RA Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y.,
RA Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A.,
RA Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,
RA Masuchi Y., Shizuya H., Kikuchi H.;
RT "Complete sequence and gene organization of the genome of a hyper-
RT thermophilic archaeobacterium, Pyrococcus horikoshii OT3.";
RL DNA Res. 5:55-76 (1998).
DR EMBL; AP000003; BAA29928.1; -.
DR PIR; F71133; F71133.
DR HSSP; P02905; 1BDO.
DR GO; GO:0009374; F:biotin binding; IEA.
DR GO; GO:0003824; F:catalytic activity; IEA.
DR GO; GO:0008948; F:oxaloacetate decarboxylase activity; IEA.
DR GO; GO:0006814; P:sodium ion transport; IEA.
DR InterPro; IPR001882; Biotin_BS.
DR InterPro; IPR000089; Biotin_lipoyl.
DR InterPro; IPR000891; HMGL-like.
DR InterPro; IPR005776; Oada.
DR InterPro; IPR003379; PYC_OADA.
DR Pfam; PF00364; biotin_lipoyl; 1.
DR Pfam; PF00682; HMGL-like; 1.
DR Pfam; PF02436; PYC_OADA; 1.
DR TIGRFAMs; TIGR01108; oada; 1.
DR PROSITE; PS00188; BIOTIN; 1.
KW Complete proteome.
SQ SEQUENCE 571 AA; 64748 MW; B308B0B1C0E5B103 CRC64;

Query Match 29.9%; Score 184; DB 17; Length 571;
Best Local Similarity 37.5%; Pred. No. 6.5e-07;
Matches 45; Conservative 24; Mismatches 43; Indels 8; Gaps 3;
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QY 3 LKVTVNGTAYDVVDV-DVKSHENPMGTILFGGGTGGAPAPAAAGGAGAGKAGEGIPAPLA 61
Db 458 IKIYINGKEFEVFEVGEIEFPPKPKQV---QAIPSQPKREVAPSGSV-----VSAPMP 510
QY 62 GTVSKILVKEGDTVKGQTVLVLEAMKMETEINAPTDGKVEKVLVKERDAVQGGQGLIKI 121
Db 511 GKVLVLVRVGDRVRVGQGLLVLEAMKMEINEIPSPRDGVVVRILVKEGEAVDTGQPLIEL 570

RESULT 18
Q8R7M0 PRELIMINARY; PRT; 122 AA.
AC Q8R7M0;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Biotin carboxyl carrier protein.
GN ACCB2 OR TTE2383.
OS Thermoanaerobacter tengcongensis.
OC Bacteria; Firmicutes; Clostridia; Thermoanaerobacteriales;
OC Thermoanaerobacteriaceae; Thermoanaerobacter.
OX NCBI_TaxID=119072;
RN [1]

SEQUENCE FROM N.A.
RC STRAIN=MB4 / JCM 11007;
RX MEDLINE=21992816; PubMed=11997336;
RA Bao Q., Tian Y., Li W., Xu Z., Xuan Z., Hu S., Dong W., Yang J.,
RA Chen Y., Xue Y., Xu Y., Lai X., Huang L., Dong X., Ma Y., Ling L.,
RA Tan H., Chen R., Wang J., Yu J., Yang H.;
RT "A complete sequence of T. tengcongensis genome.";
RL Genome Res. 12:689-700(2002).
DR EMBL; AE013180; AAM25522.1;
DR GO; GO:0009374; F:biotin binding; IEA.
DR InterPro; IPR001882; Biotin_BS.
DR InterPro; IPR000089; Biotin_lipoyl.
DR Pfam; PF00364; biotin_lipoyl; 1.
DR PROSITE; PS00188; BIOTIN; 1.
KW Complete proteome.
SQ SEQUENCE 122 AA; 13437 MW; 649BFC4629C337C5 CRC64;

Query Match 29.2%; Score 179.5; DB 16; Length 122;
Best Local Similarity 34.5%; Pred. No. 2.6e-07;
Matches 48; Conservative 12; Mismatches 36; Indels 43; Gaps 3;

QY 2 KLVTVNGTAYDVVDV-----DVKSHENPMGTILFGGGTGGAPA 40
Db 3 KFKVTVNGKTYEVEVEEMKAEKESKEEIVEVEVPKQEEK----- 46
QY 41 PAAGGAGAGKAGEGEIPAPLAGTVSKILVKEGDTVKGQTVLVLEAMKMETEINAPTDGK 100
Db 47 -----VSTGK-GSKVVSAPMPGTILDVRVKEGDRVRGVDVLLILEAMKMEINEIMAPEDGI 100
QY 101 VEKVLVKERDAVQGGQGLI 119
Db 101 VASVNVSKGASVNTGDVLV 119

RESULT 19
Q8U917 PRELIMINARY; PRT; 576 AA.
AC Q8U917;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Biotin carboxylase.
GN ATU3913 OR AGR_L1864.
OS Agrobacterium tumefaciens (strain C58 / ATCC 33970).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.
OX NCBI_TaxID=176299;
RN [1]
RP SEQUENCE FROM N.A.

RX MEDLINE=21608550; PubMed=11743193;
RA Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,
RA Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.,
RA Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr.,
RA Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,
RA Kutayavin T., Levy R., Li M.-J., McClelland E., Palmieri A., Gordon D.,
RA Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Perry M.,
RA Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M.,
RA Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,
RA Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
RA Nester E.W.;
RT "The genome of the natural genetic engineer Agrobacterium tumefaciens
C58.";
RL Science 294:2317-2323(2001).
RN [2]

SEQUENCE FROM N.A.
RX MEDLINE=21608551; PubMed=11743194;
RA Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M., Mullin L.,
RA Quorillo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Liu F.,
RA Houmiel K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F.,
RA Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B.,
RA Flanagan C., Crowell C., Gursen J., Lomo C., Sear C., Strub G.,
RA Cielo C., Slater S.;
RT "Genome sequence of the plant pathogen and biotechnology agent
Agrobacterium tumefaciens C58.";
RL Science 294:2323-2328(2001).
DR EMBL; AE009322; AAL44721.1;
DR EMBL; AE008292; AAK89506.1;
DR PIR; AC3038; AC3038.
DR PIR; H98247; H98247.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0009374; F:biotin binding; IEA.
DR GO; GO:0016874; F:ligase activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR001882; Biotin_BS.
DR InterPro; IPR005482; Biotin_carb_C.
DR InterPro; IPR000089; Biotin_lipoyl.
DR InterPro; IPR005479; CPase_L_D2.
DR InterPro; IPR005481; CPase_L_N.
DR Pfam; PF02785; Biotin_carb_C; 1.
DR Pfam; PF00364; biotin_lipoyl; 1.
DR Pfam; PF00289; CPSase_L_chain; 1.
DR Pfam; PF02786; CPSase_L_D2; 1.
DR PROSITE; PS00188; BIOTIN; 1.
DR PROSITE; PS00867; CPSASE_2; 1.
KW Complete proteome.
SQ SEQUENCE 576 AA; 61722 MW; E0299479A952581F CRC64;

Query Match 28.7%; Score 176.5; DB 16; Length 576;
Best Local Similarity 43.8%; Pred. No. 2.7e-06;
Matches 42; Conservative 17; Mismatches 28; Indels 9; Gaps 3;

QY 26 MGTILFGGGTGGAPAPAAAGGAGAGKAGEGEIPAPLAGTVSKILVKEGDTVKGQTVLVLE 85
Db 488 LGTV--SGGNASAPSAV-----EKKEGEMTAPVSGTLQSFVKVDGETVSEGDLLAVME 539
QY 86 AMKMETEINAPTDGKVEKVLVKERDAVQGGQGLIKI 121
Db 540 AMKMETQIVATRAKGV-RLIVKEGDYLOAGATLIDI 574

RESULT 20
Q9WZH6 PRELIMINARY; PRT; 134 AA.
ID Q9WZH6
AC Q9WZH6;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Propionyl-CoA carboxylase, gamma subunit.
GN TM0717.
OS Thermotoga maritima.
OC Bacteria; Thermotogae; Thermotogales; Thermotogaceae; Thermotoga.
OX NCBI_TaxID=2336;


```
QY 9 GTAYDVVDVDKS-----HENPMGTILFGGGTGGAP-----APAAGGAGA 48
Db 850 GEEIDVEIEQKTLMLVLSIGEPQPDGNGRVLVLEFNGQPREIIVKDES VKATVAQRVKG 909
QY 49 GKAGEGEIPAPLAGTVSKILVKEGDTVKGQTVLVLEAMKMETEINAPTDGKVEKVLVKE 108
Db 910 NRENPNHISATMPGTIVKVVKEGDEVKKGDSMAITEAMKMETTTVQAPFNGKVKVYVND 969
QY 109 RDAVQGGGLIKI 121
Db 970 GDAIQTGDLIEL 982
RESULT 23
Q819M9
ID Q819M9 PRELIMINARY; PRT; 1148 AA.
AC Q819M9;
DT 01-JUN-2003 (TremBLrel. 24, Created)
DT 01-JUN-2003 (TremBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TremBLrel. 25, Last annotation update)
DE Pyruvate carboxylase (EC 6.4.1.1).
GN BC3947.
OS Bacillus cereus (strain ATCC 14579 / DSM 31).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=226900;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22608415; PubMed=12721630;
RA Ivanova N., Sorokin A., Anderson I., Galleron N., Candelon B.,
RA Kapatral V., Bhattacharya A., Reznik G., Mikhailova N., Lapidus A.,
RA Chu L., Mazur M., Goltsman E., Larsen N., D'Souza M., Walunas T.,
RA Grechkin Y., Pusch G., Haselkorn R., Fonstein M., Ehrlich S.D.,
RA Overbeek R., Kyrpides N.;
RT "Genome sequence of Bacillus cereus and comparative analysis with
RT Bacillus anthracis.";
RL Nature 423:87-91(2003).
RL EMBL; AE017010; AAP10867.1; -
DR GO; GO:0005737; C:cytoplasm; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0016874; F:ligase activity; IEA.
DR GO; GO:0004736; F:pyruvate carboxylase activity; IEA.
DR GO; GO:0006094; P:gluconeogenesis; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR005482; Biotin carb C.
DR InterPro; IPR000089; Biotin_lipoyl.
DR InterPro; IPR005479; CPase_L_D2.
DR InterPro; IPR005481; CPase_L_N.
DR InterPro; IPR000891; HMGL-like.
DR InterPro; IPR003379; PYC_OADA.
DR InterPro; IPR005930; Pyruv carb.
DR Pfam; PF02785; Biotin carb_C; 1.
DR Pfam; PF00364; biotin_lipoyl; 1.
DR Pfam; PF00289; CPase_L chain; 1.
DR Pfam; PF02786; CPase_L_D2; 1.
DR Pfam; PF00682; HMGL-like; 1.
DR Pfam; PF02436; PYC_OADA; 1.
DR TIGRFAMs; TIGR01235; pyruv carb; 1.
DR PROSITE; PS00866; CPASE_1; 1.
DR PROSITE; PS00867; CPASE_2; 1.
KW Ligase; Pyruvate; Complete proteome.
SQ SEQUENCE 1148 AA; 128442 MW; EE5CC5BA99D8E191 CRC64;
Query Match 28.6%; Score 176; DB 16; Length 1148;
Best Local Similarity 33.8%; Pred. No. 6.6e-06;
Matches 45; Conservative 19; Mismatches 49; Indels 20; Gaps 2;
QY 9 GTAYDVVDVDKS-----HENPMGTILFGGGTGGAP-----APAAGGAGA 48
Db 1014 GEEIDVEIEQKTLMLVLSIGEPQPDGNGRVLVLEFNGQPREIIVKDES VKATVAQRVKG 1073
QY 49 GKAGEGEIPAPLAGTVSKILVKEGDTVKGQTVLVLEAMKMETEINAPTDGKVEKVLVKE 108
Db 1074 NRENPNHISATMPGTIVKVVKEGDEVKKGDSMAITEAMKMETTTVQAPFNGKVKVYVND 1133
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QY 109 RDAVQGGGLIKI 121
Db 1134 GDAIQTGDLIEL 1146
RESULT 24
Q82YV7
ID Q82YV7 PRELIMINARY; PRT; 133 AA.
AC Q82YV7;
DT 01-JUN-2003 (TremBLrel. 24, Created)
DT 01-JUN-2003 (TremBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TremBLrel. 25, Last annotation update)
DE Sodium ion-translocating decarboxylase, biotin carboxyl carrier
DE protein.
GN EF3325.
OS Enterococcus faecalis (Streptococcus faecalis).
OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
OX NCBI_TaxID=1351;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=V583 / ATCC 700802;
RX MEDLINE=22550857; PubMed=12663927;
RA Paulsen I.T., Banerjee L., Myers G.S.A., Nelson K.E., Seshadri R.,
RA Read T.D., Fouts D.E., Eisen J.A., Gill S.R., Heidelberg J.F.,
RA Tettelin H., Dodson R.J., Umayam L., Brinkac L., Beanan M.,
RA Daugherty S., DeBoy R.T., Durkin S., Kolonay J., Madupu R., Nelson W.,
RA Vamathevan J., Tran B., Upton J., Hansen T., Shetty J., Khouri H.,
RA Utterback T., Radune D., Ketchum K.A., Dougherty B.A., Fraser C.M.;
RT "Role of mobile DNA in the evolution of vancomycin-resistant
RT Enterococcus faecalis.";
RL Science 299:2071-2074(2003).
RL EMBL; AE016957; AAO82990.1; -
DR TIGR; EF3325; -
DR GO; GO:0009374; F:biotin binding; IEA.
DR InterPro; IPR001882; Biotin_BS.
DR InterPro; IPR000089; Biotin_lipoyl.
DR Pfam; PF00364; biotin_lipoyl; 1.
DR PROSITE; PS00188; BIOTIN; 1.
KW Complete proteome.
SQ SEQUENCE 133 AA; 13655 MW; D828752A1CIADEAF CRC64;
Query Match 28.5%; Score 175.5; DB 16; Length 133;
Best Local Similarity 37.2%; Pred. No. 6e-07;
Matches 48; Conservative 17; Mismatches 55; Indels 9; Gaps 2;
QY 2 KLKVTVNGTAYDVVD-----VDKSHENPMGTILFGGGTGGAPA----PAAGGAGAGKAG 52
Db 4 KFKISIDGKEYLVEEMEEIGGVQPAPVAPQPTAPVATTETPAPAVEETPASAAQPAAPAG 63
QY 53 EGEIPAPLAGTVSKILVKEGDTVKGQTVLVLEAMKMETEINAPTDGKVEKVLVKEKDAV 112
Db 64 ADAMPAPMPGTVLKVLNVGDTVSENQPLLLILEAMKMEINEIVAGKAGTTGTGIHVTQGOIV 123
QY 113 QGGQGLIKI 121
Db 124 NPGEPLITI 132
RESULT 25
Q88C37
ID Q88C37 PRELIMINARY; PRT; 602 AA.
AC Q88C37;
DT 01-JUN-2003 (TremBLrel. 24, Created)
DT 01-JUN-2003 (TremBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TremBLrel. 25, Last annotation update)
DE Oxaloacetate decarboxylase, alpha subunit.
GN OADA OR PP5346.
OS Pseudomonas putida (strain KT2440).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OX Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=160488;
RN [1]
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RP SEQUENCE FROM N.A.
RX MEDLINE=22423060; PubMed=12534463;
RA Nelson K.E., Weinel C., Paulsen I.T., Dodson R.J., Hilbert H.,
RA Martins dos Santos V.A.P., Fouts D.E., Gill S.R., Pop M., Holmes M.,
RA Brinkac L., Beanan M., DeBoy R.T., Daugherty S., Kolonay J.,
RA Madupu R., Nelson W., White O., Peterson J., Khouri H., Hance I.,
RA Chris Lee P., Holtzapple E., Scanlan D., Tran K., Moazzez A.,
RA Utterback T., Rizzo M., Lee K., Kosack D., Moestl D., Wedler H.,
RA Lauber J., Stjepandic D., Hoheisel J., Straetz M., Heim S.,
RA Kiewitz C., Eisen J., Timmis K.N., Duesterhoeft A., Tuemmler B.,
RA Fraser C.M.;
RT "Complete genome sequence and comparative analysis of the
RT metabolically versatile *Pseudomonas putida* KT2440.";
RL Environ. Microbiol. 4:799-808(2002).
DR EMBL; AE016794; AAN70911.1; -.
DR TIGR; PP5346; -.
DR GO; GO:0003824; F:catalytic activity; IEA.
DR GO; GO:0006520; P:amino acid metabolism; IEA.
DR InterPro; IPR000089; Biotin_lipoyl.
DR InterPro; IPR000891; HMGL-like.
DR InterPro; IPR003379; PYC OADA.
DR InterPro; IPR000634; S/T_dehydratse_BS.
DR Pfam; PF00364; biotin_lipoyl; 1.
DR Pfam; PF00682; HMGL-like; 1.
DR Pfam; PF02436; PYC OADA; 1.
DR PROSITE; PS00165; DEHYDRATASE_SER_THR; 1.
DR Complete proteome.
KW SEQUENCE 602 AA; 65626 MW; 98552963F0E691A7 CRC64;
SQ

Query Match 28.5%; Score 175.5; DB 16; Length 602;
Best Local Similarity 33.8%; Pred. No. 3.4e-06;
Matches 46; Conservative 17; Mismatches 44; Indels 29; Gaps 3;

QY 5 VTVNGTAYDVVDV-----DVKSH-----NPMGTILFGGGTGAPAPAAGG 45
Db 475 IDVHGETYRVDITGVGKAEGRHFYLSIDGMPEEVVFVFEPLNEFVSGGSKRKA----- 529

QY 46 AGAGKAGEGEIPAPLAGTIVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVL 105
Db 530 -----TDPGHVSTTTPGNIIVLVKEGDMVKAGQAVLITEAMKMETEVQAIAIGKVVAIH 584

QY 106 VKERDAVQGGQGLIKI 121
Db 585 VAKGDRVTPGEILLIEI 600

RESULT 26
Q9HPP8 PRELIMINARY; PRT; 610 AA.
AC Q9HPP8;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Biotin carboxylase.
GN ACC OR VNGI532G.
OS Halobacterium sp. (strain NRC-1 / ATCC 700922 / JCM 11081).
OC Archaea; Euryarchaeota; Halobacteria; Halobacteriales;
OC Halobacteriaceae; Halobacterium.
OX NCBI_TaxID=64091;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20504483; PubMed=11016950;
RA Ng W.V., Kennedy S.P., Mahairas G.G., Berquist B., Pan M.,
RA Shukla H.D., Lasky S.R., Baliga N.S., Thorsson V., Sbrogna J.,
RA Swartzell S., Weir D., Hall J., Dahl T.A., Welti R., Goo Y.A.,
RA Leithauser B., Keller K., Cruz R., Danson M.J., Hough D.W.,
RA Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H.,
RA Isenbarger T.A., Peck R.F., Pohlschroder M., Spudich J.L., Jung K.-H.,
RA Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,
RA Ebhardt H., Lowe T.M., Liang P., Riley M., Hood L., DasSarma S.;
RT "Genome sequence of Halobacterium species NRC-1.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).
DR EMBL; AE005066; AAG19819.1; -.

DR PIR; G84306; G84306.
DR HSSP; P24182; 1BNC.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0009374; F:biotin binding; IEA.
DR GO; GO:0016874; F:Ligase activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR001882; Biotin_BS.
DR InterPro; IPR005482; Biotin_carb_C.
DR InterPro; IPR000089; Biotin_lipoyl.
DR InterPro; IPR005479; CPase_L_D2.
DR InterPro; IPR005481; CPase_L_N.
DR Pfam; PF02785; Biotin_carb_C; 1.
DR Pfam; PF00364; biotin_lipoyl; 1.
DR Pfam; PF00289; CPSase_L_chain; 1.
DR Pfam; PF02786; CPSase_L_D2; 1.
DR PROSITE; PS00188; BIOTIN; 1.
DR PROSITE; PS00867; CPSASE_2; 1.
KW Complete proteome.
SQ SEQUENCE 610 AA; 65805 MW; FC586D84382DD6F2 CRC64;

Query Match 28.5%; Score 175.5; DB 17; Length 610;
Best Local Similarity 38.1%; Pred. No. 3.5e-06;
Matches 48; Conservative 18; Mismatches 43; Indels 17; Gaps 5;

QY 5 VTVNGTAYDVVDVVDKSHENPMGTILFGG-----GTGGAPAPAAGGAGAGKA---GEGE- 55
Db 492 VEVNGKRFEVNL-----ERGAAQFAAPEADTGGGPPPEP-AGGADDDGETVVEGDGET 543

QY 56 IPAPLAGTIVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVLKERDAVQGG 115
Db 544 VTAEMQGTILDVAVSEGDAVDAGDVLVLEAMKMEVDVAVSHGGTGTQVAVSEDDSDVDMD 603

QY 116 QGLIKI 121
Db 604 DVLVVI 609

RESULT 27
Q81MT6 PRELIMINARY; PRT; 1148 AA.
ID Q81MT6
AC Q81MT6;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Pyruvate carboxylase.
GN PYC OR BA4157.
OS Bacillus anthracis (strain Ames).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=198094;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22608414; PubMed=12721629;
RA Read T.D., Peterson S.N., Tourasse N., Baillie L.W., Paulsen I.T.,
RA Nelson K.E., Tettelin H., Fouts D.E., Eisen J.A., Gill S.R.,
RA Holtzapple E.K., Okstad O.A., Helgason E., Rilstone J., Wu M.,
RA Kolonay J.F., Beanan M.J., Dodson R.J., Brinkac L.M., Gwinn M.,
RA DeBoy R.T., Madpu R., Daugherty S.C., Durkin A.S., Haft D.H.,
RA Nelson W.C., Peterson J.D., Pop M., Khouri H.M., Radune D.,
RA Benton J.L., Mahamoud Y., Jiang L., Hance I.R., Weidman J.F.,
RA Berry K.J., Plaut R.D., Wolf A.M., Watkins K.L., Nierman W.C.,
RA Hazen A., Cline R., Redmond C., Thwaite J.E., White O., Salzberg S.L.,
RA Thomason B., Friedlander A.M., Koehler T.M., Hanna P.C., Kolsto A.-B.,
RA Fraser C.M.;
RT "The genome sequence of *Bacillus anthracis* Ames and comparison to
RT closely related bacteria.";
RL Nature 423:81-86(2003).
DR EMBL; AE017037; AAP27881.1; -.
DR TIGR; BA4157; -.
DR GO; GO:0005737; C:cytoplasm; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0016874; F:Ligase activity; IEA.
DR GO; GO:0004736; F:pyruvate carboxylase activity; IEA.
DR GO; GO:0006094; P:gluconeogenesis; IEA.

DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR005482; Biotin_carb_C.
DR InterPro; IPR000089; Biotin_lipoyl.
DR InterPro; IPR005479; CPase_L_D2.
DR InterPro; IPR005481; CPase_L_N.
DR InterPro; IPR000891; HMGL-like.
DR InterPro; IPR003379; PYC_OADA.
DR InterPro; IPR005930; Pyruv_carbox.
DR Pfam; PF02785; Biotin_carb_C; 1.
DR Pfam; PF00364; biotin_lipoyl; 1.
DR Pfam; PF00289; CPSase_L_chain; 1.
DR Pfam; PF02786; CPSase_L_D2; 1.
DR Pfam; PF00682; HMGL-like; 1.
DR Pfam; PF02436; PYC_OADA; 1.
DR TIGRFAMS; TIGR01235; pyruv_carbox; 1.
DR PROSITE; PS00866; CPSASE_1; 1.
DR PROSITE; PS00867; CPSASE_2; 1.
KW Pyruvate; Complete proteome.
SQ SEQUENCE 1148 AA; 128573 MW; 57B97F8D9D1287BF CRC64;

Query Match 28.5%; Score 175; DB 16; Length 1148;
Best Local Similarity 45.1%; Pred. No. 7.9e-06;
Matches 37; Conservative 14; Mismatches 31; Indels 0; Gaps 0;

QY 40 APAAGGAGAGKAGEGEIPAPLAGTQSVKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDG 99
Db 1065 ATVAQRVKGRENPNHISATMPGTIVKVVVKEGDEVKKGDSMAITEAMKMETTVQAPFNG 1124

QY 100 KVEKVLVKERDAVQGGGLIKI 121
Db 1125 KVKKVYVNDGDAIQGDLLEL 1146

RESULT 28
Q8FRP0 ID Q8FRP0 PRELIMINARY; PRT; 456 AA.
AC Q8FRP0;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Acyl-CoA carboxylase.
GN ACCBC OR CE0719.
OS Corynebacterium efficiens.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Corynebacteriaceae; Corynebacterium.
OX NCBI_TaxID=152794;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=YS-314 / AJ 12310 / DSM 44549 / JCM 11189;
RA Kwarabayasi Y., Yamazaki J., Hino Y., Kikuchi H., Nakamura Y.,
RA Ikeo K., Suzuki M., Mashima J., Itoh T., Yamagishi A., Nishio Y.,
RA Usuda Y., Sugimoto S.;
RT "The entire genomic sequence of Corynebacterium efficiens YS-314.";
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMEL; AP005216; BAC17529.1; -.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0009374; F:biotin binding; IEA.
DR GO; GO:0016874; F:ligase activity; IEA.
DR InterPro; IPR001882; Biotin_BS.
DR InterPro; IPR005482; Biotin_carb_C.
DR InterPro; IPR000089; Biotin_lipoyl.
DR Pfam; PF02785; Biotin_carb_C; 1.
DR Pfam; PF00364; biotin_lipoyl; 1.
DR Pfam; PF02786; CPSase_L_D2; 1.
DR PROSITE; PS00188; BIOTIN; 1.
DR PROSITE; PS00867; CPSASE_2; 1.
KW Complete proteome.
SQ SEQUENCE 456 AA; 48958 MW; 748919EAC7679EE0 CRC64;

Query Match 28.3%; Score 174; DB 16; Length 456;
Best Local Similarity 36.3%; Pred. No. 3.3e-06;
Matches 45; Conservative 20; Mismatches 45; Indels 14; Gaps 3;

QY 2 KLKVTVNGTAYDVVDVVDKSHENPMGTILFGGGTGGAPAP-----AAGGAGAGKAGEGEIP 57
Db 342 KVIVEIDGRRRVEVALP-----GDALGGGAGAAKKPKRRAGGAKGVSGD-SVA 391

QY 58 APLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVLVKERDAVQGGQG 117
Db 392 APMQGTIVKVNVEDGAEVSEGDVVVLEAMKMPVKAHKSGTVSGLTIAAGEGVTKGQV 451

QY 118 LIKI 121
Db 452 LLEI 455

RESULT 29
Q8RQN4 ID Q8RQN4 PRELIMINARY; PRT; 591 AA.
AC Q8RQN4;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Acyl-CoA carboxylase B and C subunit.
GN ACCBC.
OS Corynebacterium efficiens.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Corynebacteriaceae; Corynebacterium.
OX NCBI_TaxID=152794;
RN [1]
RP SEQUENCE FROM N.A.
RA Hirano S., Kimura E., Kawahara Y., Sugimoto S.;
RT "accBC of Corynebacterium efficiens.";
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
CC -I- COFACTOR: BIOTIN (BY SIMILARITY).
DR EMBL; AB083052; BAB88668.1; -.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0009374; F:biotin binding; IEA.
DR GO; GO:0016874; F:ligase activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR001882; Biotin_BS.
DR InterPro; IPR005482; Biotin_carb_C.
DR InterPro; IPR000089; Biotin_lipoyl.
DR InterPro; IPR005479; CPase_L_D2.
DR InterPro; IPR005481; CPase_L_N.
DR Pfam; PF02785; Biotin_carb_C; 1.
DR Pfam; PF00364; biotin_lipoyl; 1.
DR Pfam; PF00289; CPSase_L_chain; 1.
DR Pfam; PF02786; CPSase_L_D2; 1.
DR PROSITE; PS00188; BIOTIN; 1.
DR PROSITE; PS00867; CPSASE_2; 1.
KW Biotin.
SQ SEQUENCE 591 AA; 63256 MW; 345BCEC36C5D8ACA CRC64;

Query Match 28.3%; Score 174; DB 2; Length 591;
Best Local Similarity 36.3%; Pred. No. 4.4e-06;
Matches 45; Conservative 20; Mismatches 45; Indels 14; Gaps 3;

QY 2 KLKVTVNGTAYDVVDVVDKSHENPMGTILFGGGTGGAPAP-----AAGGAGAGKAGEGEIP 57
Db 477 KVIVEIDGRRRVEVALP-----GDALGGGAGAAKKPKRRAGGAKGVSGD-SVA 526

QY 58 APLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVLVKERDAVQGGQG 117
Db 527 APMQGTIVKVNVEDGAEVSEGDVVVLEAMKMPVKAHKSGTVSGLTIAAGEGVTKGQV 586

QY 118 LIKI 121
Db 587 LLEI 590

RESULT 30
Q8K7F5 ID Q8K7F5 PRELIMINARY; PRT; 131 AA.
AC Q8K7F5;

DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Putative decarboxylase gamma chain.
GN SPYM3 0830.
OS Streptococcus pyogenes (serotype M3).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=198466;
RN [1]
RC STRAIN=MGAS315 / Serotype M3;
RX MEDLINE=22133808; PubMed=12122206;
RA Beres S.B., Sylva G.L., Barbican K.D., Lei B., Hoff J.S.,
RA Mammarella N.D., Liu M.-Y., Smoot J.C., Porcella S.F., Parkins L.D.,
RA Campbell D.S., Smith T.M., McCormick J.K., Leung D.Y.M.,
RA Schlievert P.M., Musser J.M.;
RT "Genome sequence of a serotype M3 strain of group A Streptococcus:
RT phage-encoded toxins, the high-virulence phenotype, and clone
RT emergence";
RL Proc. Natl. Acad. Sci. U.S.A. 99:10078-10083 (2002).
DR EMBL; AE014153; AAM79437.1; --
DR GO; GO:0009374; F:biotin binding; IEA.
DR InterPro; IPR001882; Biotin_BS.
DR InterPro; IPR001882; Biotin_BS.
DR InterPro; IPR000089; Biotin_lipoyl.
DR Pfam; PF00364; biotin_lipoyl; 1.
DR PROSITE; PS00188; BIOTIN; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 131 AA; 13397 MW; 2FFD88C2487FB29E CRC64;

Query Match 28.2%; Score 173.5; DB 16; Length 131;
Best Local Similarity 32.4%; Pred. No. 8.5e-07;
Matches 47; Conservative 15; Mismatches 42; Indels 41; Gaps 2;

QY 2 KLKVTVNGTAYDVVDVDKSHENPMGTILFGGGTGGAPAPAGGA----- 46
Db 4 KFKITIDGKEYLVEME-----EIGAPAQAAPAPQISTPVPVPTTEASP 46

QY 47 -----GAGKAGEGEIPAPLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPT 97
Db 47 QVEEAQAPQPVAAAGADAIPSPMPGTILKVLVAVGDQVTENQPLLILEAMKMEINEIVASS 106

QY 98 DGKVEKVLVKERDAVQGGGLIKIG 122
Db 107 AGTITAIHVGPQGVNPGDGLITIG 131

RESULT 31
Q99ZL1
ID Q99ZL1 PRELIMINARY; PRT; 132 AA.
AC Q99ZL1;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Putative decarboxylase, gamma chain.
GN SPY1183.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RC STRAIN=SF370 / ATCC 700294 / Serotype M1;
RX MEDLINE=21192684; PubMed=11296296;
RA Ferretti J.J., McShan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K.,
RA Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P.,
RA Qian Y., Jia H.G., Najjar F.Z., Ren Q., Zhu H., Song L., White J.,
RA Yuan X., Clifton S.W., Roe B.A., McLaughlin R.;
RT "Complete genome sequence of an M1 strain of Streptococcus pyogenes.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663 (2001).
CC -1- COFACTOR: BIOTIN (BY SIMILARITY).
DR EMBL; AE006559; AAK34049.1; --
DR HSSP; P02905; 3BDO.

DR GO; GO:0009374; F:biotin binding; IEA.
DR InterPro; IPR001882; Biotin_BS.
DR InterPro; IPR000089; Biotin_lipoyl.
DR Pfam; PF00364; biotin_lipoyl; 1.
DR PROSITE; PS00188; BIOTIN; 1.
KW Biotin; Complete proteome.
SQ SEQUENCE 132 AA; 13529 MW; 2FA2B1FB8119429E CRC64;

Query Match 28.2%; Score 173.5; DB 16; Length 132;
Best Local Similarity 32.4%; Pred. No. 8.6e-07;
Matches 47; Conservative 15; Mismatches 42; Indels 41; Gaps 2;

QY 2 KLKVTVNGTAYDVVDVDKSHENPMGTILFGGGTGGAPAPAGGA----- 46
Db 5 KFKITIDGKEYLVEME-----EIGAPAQAAPAPQISTPVPVPTTEASP 47

QY 47 -----GAGKAGEGEIPAPLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPT 97
Db 48 QVEEAQAPQPVAAAGADAIPSPMPGTILKVLVAVGDQVTENQPLLILEAMKMEINEIVASS 107

QY 98 DGKVEKVLVKERDAVQGGGLIKIG 122
Db 108 AGTITAIHVGPQGVNPGDGLITIG 132

RESULT 32
Q97VY7
ID Q97VY7 PRELIMINARY; PRT; 186 AA.
AC Q97VY7;
DT 01-OCT-2001 (TrEMBLrel. 18, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Biotin carboxyl carrier protein of propionyl-CoA carboxylase beta
DE subunit (EC 6.4.1.3).
GN SSO2464.
OS Sulfolobus solfataricus.
OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
OC Sulfolobus.
OX NCBI_TaxID=2287;
RN [1]
RC STRAIN=ATCC 35092 / DSM 1617 / P2;
RX MEDLINE=21332296; PubMed=11427726;
RA She Q., Singh R.K., Confalonieri F., Zivanovic Y., Allard G.,
RA Awayez M.J., Chan-Weiher C.C.-Y., Clausen I.G., Curtis B.A.,
RA De Moors A., Brauso G., Fletcher C., Gordon P.M.K.,
RA Heikamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., Peng X.,
RA Thi-Ngoc H.P., Redder P., Schenk M.E., Theriault C., Tolstrup N.,
RA Charlebois R.L., Doolittle W.F., Duguet M., Gaasterland T.,
RA Garrett R.A., Ragan M.A., Sensen C.W., Van der Oost J.;
RT "The complete genome of the crenarchaeon Sulfolobus solfataricus P2.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:7835-7840 (2001).
DR EMBL; AE006845; AAK42603.1; --
DR PIR; D90418; D90418.
DR GO; GO:0009374; F:biotin binding; IEA.
DR GO; GO:0016874; F:ligase activity; IEA.
DR GO; GO:0004658; F:propionyl-CoA carboxylase activity; IEA.
DR InterPro; IPR001882; Biotin_BS.
DR InterPro; IPR000089; Biotin_lipoyl.
DR Pfam; PF00364; biotin_lipoyl; 1.
DR PROSITE; PS00188; BIOTIN; 1.
KW Ligase; Complete proteome.
SQ SEQUENCE 186 AA; 21166 MW; DB26587C39883B08 CRC64;

Query Match 28.2%; Score 173.5; DB 17; Length 186;
Best Local Similarity 40.0%; Pred. No. 1.3e-06;
Matches 50; Conservative 14; Mismatches 42; Indels 19; Gaps 4;

QY 7 VNGTAYDVVDVDKSHENPMGTILFGGG-----TGGAPAPAGGAGA-----GKAGEGEI 56
Db 70 INGKKYVVFIESD-----GTLIFNHQDFLRDKVTEIPKGEERVEEIRGK--EGEI 120

QY 57 PAPLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTGDGKVEKVLVKERDAVQGGQ 116

Db 121 VSPFLGRVVKIRVKEGDAVNKGQPLLSIEAMKAETVVISSPIGGIVQKILIKEGGQVKKGD 180
QY 117 GLIKI 121
Db 181 ILIVI 185

RESULT 33
Q8XGX8 PRELIMINARY; PRT; 591 AA.
AC Q8XGX8;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Oxaloacetate decarboxylase alpha chain (EC 4.1.1.3).
GN OADA OR SV3532 OR T0057 OR T3267.
OS Salmonella typhi.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_TaxID=601;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CT18;
RX MEDLINE=21534947; PubMed=11677608;
RA parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
RA Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebahia M.,
RA Baker S., Basham D., Brooks K., Chillingworth T., Connerton P.,
RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
RA Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K.,
RA Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,
RA Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,
RA Whitehead S., Barrell B.G.;
RT "Complete genome sequence of a multiple drug resistant Salmonella
enterica serovar Typhi CT18.";
RL Nature 413:848-852(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Ty2 / ATCC 700931;
RX MEDLINE=22531367; PubMed=12644504;
RA Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
RA Burland V., Kodoyianni V., Schwartz D.C., Blattner F.R.;
RT "Comparative genomics of Salmonella enterica serovar Typhi strains Ty2
and CT18.";
RL J. Bacteriol. 185:2330-2337(2003).
DR EMBL; AL627278; CAD07867.1; -
DR EMBL; AL627265; CAD01210.1; -
DR EMBL; AE016834; AAO67790.1; -
DR EMBL; AE016845; AAO70802.1; -
DR GO; GO:0009374; F:biotin binding; IEA.
DR GO; GO:0016829; F:lyase activity; IEA.
DR GO; GO:0008948; F:oxaloacetate decarboxylase activity; IEA.
DR GO; GO:0006814; P:sodium ion transport; IEA.
DR InterPro; IPR001882; Biotin_BS.
DR InterPro; IPR000089; Biotin_lipoyl.
DR InterPro; IPR000891; HMGL-like.
DR InterPro; IPR005776; Oada.
DR Pfam; PF003379; PYC_OADA.
DR Pfam; PF00364; biotin_lipoyl; 1.
DR Pfam; PF00682; HMGL-like; 1.
DR Pfam; PF02436; PYC_OADA; 1.
DR TIGRFAMs; TIGR01108; oada; 1.
DR PROSITE; PS00188; BIOTIN; 1.
KW Lyase; Complete proteome.
SQ SEQUENCE 591 AA; 53372 MW; 10F3A3BE94AB7DD2 CRC64;

Query Match 28.2%; Score 173.5; DB 16; Length 591;
Best Local Similarity 40.2%; Pred. No. 4.9e-06;
Matches 47; Conservative 14; Mismatches 49; Indels 7; Gaps 3;
QY 5 VTVNGTAYDVVDVKSHENPMGTILFGGTGGAPAPAGGAGAGKAGAGEIPAPLAGIV 64
Db 481 VEVEGKAFVVRVS-DGGDISQLTTAV--FAASSAPVQAAAPAGAGT-----PVTAPLAGNI 533

QY 65 SKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVLVKERDAVQGGQGLIKI 121
Db 534 WKVIATEGQSVAGEDVLLILEAMKMETEIRAAQAGTVRGIAVKSGDAVSVGDTLMTL 590
RESULT 34
Q87U07 PRELIMINARY; PRT; 602 AA.
AC Q87U07;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Oxaloacetate decarboxylase, alpha subunit.
GN OADA OR PSPTO5510.
OS Pseudomonas syringae (pv. tomato).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=323;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DC3000;
RA Buell R., Joardar V., Khouri H., Fedorova N., Tran B., Russell D.,
RA Berry K., Utterback T., Van Aken S., Feldblyum T., Gwinn M.,
RA Dodson R., DeBoy R., Durkin A., Kolonay J., Madupu R., Daugherty S.,
RA Brinkac L., Beanan M., Haft D., Selengut J., Nelson W., Davidsen T.,
RA White O., Fraser C., Collmer A.;
RT "Complete sequence of Pseudomonas syringae.";
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE016876; AAO58929.1; -
DR TIGR; PSPTO5510; -
DR GO; GO:0003824; F:catalytic activity; IEA.
DR GO; GO:0006520; P:amino acid metabolism; IEA.
DR InterPro; IPR000089; Biotin_lipoyl.
DR InterPro; IPR000891; HMGL-like.
DR InterPro; IPR003379; PYC_OADA.
DR InterPro; IPR00634; S/T_dehydrtse_BS.
DR Pfam; PF00364; biotin_lipoyl; 1.
DR Pfam; PF00682; HMGL-like; 1.
DR Pfam; PF02436; PYC_OADA; 1.
DR PROSITE; PS00165; DEHYDRATASE_SER_THR; 1.
KW Complete proteome.
SQ SEQUENCE 602 AA; 65598 MW; BD644376294712E3 CRC64;
Query Match 28.0%; Score 172.5; DB 16; Length 602;
Best Local Similarity 33.1%; Pred. No. 6e-06;
Matches 45; Conservative 18; Mismatches 44; Indels 29; Gaps 3;
QY 5 VTVNGTAYDVVDV-----DVDKSHE-----NPMGTILFGGTGGAPAPAGG 45
Db 475 IDVHGETYRVDITGVGVKAEGKRHFYLTIDGMPEEVVFEPLNEFVGGASKRQASA--- 531
QY 46 AGAGKAGEGEIPAPLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVL 105
Db 532 -----PGHVSTTMPGNIVDVLVKEGDVVKAGQAVLITEAMKMETEVQASTAGKVVAIH 584
QY 106 VKERDAVQGGQGLIKI 121
Db 585 VAKGDRVNPGEILVEI 600
RESULT 35
Q8R5Y8 PRELIMINARY; PRT; 134 AA.
AC Q8R5Y8;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Biotin carboxyl carrier protein of glutaconyl-CoA decarboxylase
DE (EC 4.1.1.70).
GN FN0200.
OS Fusobacterium nucleatum (subsp. nucleatum).
OC Bacteria; Fusobacteria; Fusobacteriales; Fusobacteriaceae;

OC Fusobacterium.
OX NCBI_TaxID=76856;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 25586;
RX MEDLINE=21886394; PubMed=11889109;
RA Kapatal V., Anderson I., Ivanova N., Reznik G., Los T., Lykidis A.,
RA Bhattacharyya A., Bartman A., Gardner W., Grechkin G., Zhu L.,
RA Vasieva O., Chu L., Kogan Y., Chaga O., Goltzman E., Bernal A.,
RA Larsen N., D'Souza M., Walunas T., Pusch G., Haselkorn R.,
RA Fonstein M., Kyrpides N., Overbeek R.,
RT "Genome sequence and analysis of the oral bacterium Fusobacterium
RT nucleatum strain ATCC 25586.";
RL J. Bacteriol. 184:2005-2018(2002).
DR EMBL; AE010533; AAL94406.1; -.
DR GO; GO:0009374; F:biotin binding; IEA.
DR GO; GO:0018801; F:glutacetyl-CoA decarboxylase activity; IEA.
DR GO; GO:0016829; F:lyase activity; IEA.
DR InterPro; IPR001882; Biotin_BS.
DR InterPro; IPR000089; Biotin_lipoyl.
DR Pfam; PF00364; biotin_lipoyl; 1.
DR PROSITE; PS00188; BIOTIN; 1.
KW Lyase; Complete proteome.
SQ SEQUENCE 134 AA; 14063 MW; 177943F669196AC6 CRC64;

Query Match 28.0%; Score 172; DB 16; Length 134;
Best Local Similarity 34.8%; Pred. No. 1.2e-06;
Matches 46; Conservative 20; Mismatches 52; Indels 14; Gaps 2;

QY 1 MKLKVTVNGTAYDVVDV-----VDKSHENPMGTILFGGTTGGGAPAPAGGAG 47
Db 1 MKYVVTVNGKFEVEVEKVGAGKSLRQPVRETIVVKSEPVVETKVAAPVEAAPAT 60

QY 48 AGKAGEGEIPAPLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVLVK 107
Db 61 ATTTGGT-TITSPMPGSIIDVKVNVGDKVKFGQTLAILEAMKMENDIPATADGEVAEIRVK 119

QY 108 ERDAVQGGQGLI 119
Db 120 KGDVVETDSVLI 131

RESULT 36
Q88VC5 PRELIMINARY; PRT; 1144 AA.
AC Q88VC5;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Pyruvate carboxylase (EC 6.4.1.1).
GN PYCA OR LP_2136.
OS Lactobacillus plantarum.
OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
OC Lactobacillus.
OX NCBI_TaxID=1590;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NCIMB 8826 / WCFS1;
RX MEDLINE=22480296; PubMed=12566566;
RA Kleerebezem M., Boekhorst J., van Kranenburg R., Molenaar D.,
RA Kuipers O.P., Leer R., Tarchini R., Peters S.A., Sandbrink H.M.,
RA Fiers M.W.E.J., Stiekema W., Klein Lankhorst R.M., Bron P.A.,
RA Hoffer S.M., Nierop Groot M.N., Kerkhoven R., De Vries M., Ursing B.,
RA De Vos W.M., Siezen R.J.;
RT "Complete genome sequence of Lactobacillus plantarum WCFS1.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:1990-1995(2003).
DR EMBL; AL935258; CAD64497.1; -.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0008716; F:D-alanine-D-alanine ligase activity; IEA.
DR GO; GO:0016874; F:ligase activity; IEA.
DR GO; GO:0004736; F:pyruvate carboxylase activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR GO; GO:0009252; P:peptidoglycan biosynthesis; IEA.

DR InterPro; IPR005482; Biotin_carb_C.
DR InterPro; IPR000089; Biotin_lipoyl.
DR InterPro; IPR005479; CPase_L_D2.
DR InterPro; IPR005481; CPase_L_N.
DR InterPro; IPR000291; Dala_lig_Van.
DR InterPro; IPR000891; HMGL-like.
DR InterPro; IPR003379; PYC_OADA.
DR Pfam; PF02785; Biotin_carb_C; 1.
DR Pfam; PF00364; biotin_lipoyl; 1.
DR Pfam; PF00289; CPSase_L_chain; 1.
DR Pfam; PF02786; CPSase_L_D2; 1.
DR Pfam; PF01820; Dala_Dala_ligas; 1.
DR Pfam; PF00682; HMGL-like; 1.
DR Pfam; PF02436; PYC_OADA; 1.
DR PROSITE; PS00866; CPSASE_1; 1.
DR PROSITE; PS00867; CPSASE_2; 1.
KW Ligase; Complete proteome.
SQ SEQUENCE 1144 AA; 127299 MW; BF8AFA8AD6325DCDF CRC64;

Query Match 27.9%; Score 171.5; DB 16; Length 1144;
Best Local Similarity 34.5%; Pred. No. 1.5e-05;
Matches 41; Conservative 20; Mismatches 41; Indels 17; Gaps 1;

QY 3 LKVTVNGTAYDVVDVVDKSHENPMGTILFGGTTGGGAPAPAGGAGKAGEGEIPAPLAG 62
Db 1040 LYFSINGQNEIMVKONAIHQSAITST-----RKAEPNTNEDEVGATMSG 1082

QY 63 TVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVLVKERDAVQGGQGLIKI 121
Db 1083 SVLKLLVKKGTQVKKGEPLLVTEAMKMETTIOAPEDGVIEHIYVNVAGDVIQTDDLLLEI 1141

RESULT 37
Q87LR7 PRELIMINARY; PRT; 595 AA.
ID Q87LR7
AC Q87LR7;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Oxaloacetate decarboxylase, alpha subunit.
GN VP2544.
OS Vibrio parahaemolyticus.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=670;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RIMD 2210633 / Serotype O3:K6;
RX MEDLINE=22508454; PubMed=12620739;
RA Makino K., Oshima K., Kurokawa K., Yokoyama K., Uda T., Tagomori K.,
RA Iijima Y., Najima M., Nakano M., Yamashita A., Kubota Y., Kimura S.,
RA Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.;
RT "Genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism
RT distinct from that of V. cholerae.";
RL Lancet 361:743-749(2003).
DR EMBL; AP005081; BAC60807.1; -.
DR GO; GO:0009374; F:biotin binding; IEA.
DR GO; GO:0003824; F:catalytic activity; IEA.
DR InterPro; IPR001882; Biotin_BS.
DR InterPro; IPR000089; Biotin_lipoyl.
DR InterPro; IPR000891; HMGL-like.
DR Pfam; PF00364; biotin_lipoyl; 1.
DR Pfam; PF00682; HMGL-like; 1.
DR Pfam; PF02436; PYC_OADA; 1.
DR PROSITE; PS00188; BIOTIN; 1.
KW Complete proteome.
SQ SEQUENCE 595 AA; 64275 MW; 0DC581EFBA22F0A CRC64;

Query Match 27.8%; Score 171; DB 16; Length 595;
Best Local Similarity 37.6%; Pred. No. 7.9e-06;
Matches 44; Conservative 15; Mismatches 50; Indels 8; Gaps 2;

QY 5 VTVNGTAYDVDVDKSHENPMGTILFGGTGGAPAPAAAGGAGAGKAGEGEIPAPLAGTV 64
Db 486 VRVDGQVVEVEV-----GPKGQ-LTSVTPSSASVPVAAPVAPVTTNAESVPAPLAGNI 537
QY 65 SKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVLVKERDAVQGGGLIKI 121
Db 538 FKNVQPGAEVAGDVLLILEAMKMETEIVRAARGGIVQELNVKEGDAVTVGAPLLSL 594

RESULT 38
P71122 PRELIMINARY; PRT; 591 AA.
AC P71122;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Acyl coenzyme A carboxylase (EC 6.3.4.14).
GN ACCBC OR CGL0700.
OS Corynebacterium glutamicum (Brevibacterium flavum).
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Corynebacteriaceae; Corynebacterium.
OX NCBI_TaxID=1718;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 13032; PubMed=8772169;
RX MEDLINE=96337861; PubMed=8772169;
RA Jager W., Peters-Wendisch P.G., Kalinowski J., Puhler A.;
RT "A Corynebacterium glutamicum gene encoding a two-domain protein
RT similar to biotin carboxylases and biotin-carboxyl-carrier proteins.";
RL Arch. Microbiol. 166:76-82(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 13032;
RA Jaeger W.;
RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;
RA Nakagawa S.;
RT "Complete genomic sequence of Corynebacterium glutamicum ATCC 13032.";
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
CC -!- COFACTOR: BIOTIN (BY SIMILARITY).
DR EMBL; U35023; AAB40890.1; -;
DR EMBL; AP005276; BAB98093.1; -;
DR HSSP; P24182; 1BNC.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0009374; F:biotin binding; IEA.
DR GO; GO:0004075; F:biotin carboxylase activity; IEA.
DR GO; GO:0016874; F:ligase activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR001882; Biotin_BS.
DR InterPro; IPR005482; Biotin_carb_C.
DR InterPro; IPR000089; Biotin_lipoyl.
DR InterPro; IPR005479; CPase_L_D2.
DR InterPro; IPR005481; CPase_L_N.
DR Pfam; PF02785; Biotin_carb_C; 1.
DR Pfam; PF00364; biotin_lipoyl; 1.
DR Pfam; PF00289; CPSase_L_chain; 1.
DR Pfam; PF02786; CPSase_L_D2; 1.
DR PROSITE; PS00188; BIOTIN; 1.
DR PROSITE; PS00867; CPSASE_2; 1.
KW Biotin; Ligase; Complete proteome.
SQ SEQUENCE 591 AA; 63419 MW; 0C9ED9DE184F8EF4 CRC64;

Query Match 27.7%; Score 170.5; DB 16; Length 591;
Best Local Similarity 38.7%; Pred. No. 8.6e-06;
Matches 48; Conservative 16; Mismatches 45; Indels 15; Gaps 3;
QY 2 KLKVTVNGTAYDVDVDKSHENPMGTILFGGTGGAPAPA---AGGAGAGKAGEGEIP 57
Db 478 KVVVEINGRRVEVALPGD-----LALGGTAGPKKAKRRRAGGAKAGVSGDA-VA 526
QY 58 APLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVLVKERDAVQGGQ 117

Db 527 APMQGTVIKVNVEEGAENVNEGDTVVVLEAMKMENPVKAHKS GTVTGLTVAAGEGVNKGVV 586
QY 118 LJKI 121
Db 587 LLEI 590
RESULT 39
Q8DC43 PRELIMINARY; PRT; 596 AA.
AC Q8DC43;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Pyruvate carboxylase.
GN VV11601.
OS Vibrio vulnificus.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=672;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CMCP6;
RA Rhee J.H., Kim S.Y., Chung S.S., Kim J.J., Moon Y.H., Jeong H.,
RA Choy H.E.;
RT "Complete genome sequence of Vibrio vulnificus CMCP6.";
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE016802; AAC10022.1; -;
DR GO; GO:0009374; F:biotin binding; IEA.
DR GO; GO:0003824; F:catalytic activity; IEA.
DR GO; GO:0008948; F:oxaloacetate decarboxylase activity; IEA.
DR GO; GO:0006814; P:sodium ion transport; IEA.
DR InterPro; IPR001882; Biotin_BS.
DR InterPro; IPR000089; Biotin_lipoyl.
DR InterPro; IPR000891; HMGL-like.
DR InterPro; IPR005776; Oada.
DR InterPro; IPR003379; PYC_OADA.
DR Pfam; PF00364; biotin_lipoyl; 1.
DR Pfam; PF00682; HMGL-like; 1.
DR Pfam; PF02436; PYC_OADA; 1.
DR TIGRFAMS; TIGR01108; oada; 1.
DR PROSITE; PS00188; BIOTIN; 1.
KW Complete proteome.
SQ SEQUENCE 596 AA; 64248 MW; B93B204BE2DC74F3 CRC64;
Query Match 27.7%; Score 170.5; DB 16; Length 596;
Best Local Similarity 39.2%; Pred. No. 8.7e-06;
Matches 47; Conservative 15; Mismatches 53; Indels 5; Gaps 3;
QY 7 VNGT--AYDVDVDVDKSH--ENPMGTIL-FGGGTGGAPAPAAAGGAGAGKAGEGEIPAPLA 61
Db 476 VNGAVEAYSVRVDGQVFHVEVGEGQLTSVTPAAAPASAPIAAPVSAVPSDAEAVSAPLA 535
QY 62 GTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVLVKERDAVQGGGLIKI 121
Db 536 GNIFKVHVQAGSSVEEGDILLILEAMKMETEIVRAARSGVVHVLNVKEGDAVTVGSPLLSL 595
RESULT 40
Q97FR7 PRELIMINARY; PRT; 1144 AA.
AC Q97FR7;
DT 01-OCT-2001 (TrEMBLrel. 18, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Pyruvate carboxylase, PYKA.
GN CAC2660.
OS Clostridium acetobutylicum.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1488;
RN [1]


```

SEQUENCE FROM N.A.
STRAIN=ATCC 824 / DSM 792 / VKM B-1787;
MEDLINE=21359325; PubMed=11466286;
Noelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q.,
Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I.,
Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J.,
Bennett G.N., Koonin E.V., Smith D.R.;
"Genome sequence and comparative analysis of the solvent-producing
bacterium Clostridium acetobutylicum.";
J. Bacteriol. 183:4823-4838(2001).
EMBL; AE007763; AAK80607.1; -.
PIR; D97227; D97227.
GO; GO:0005737; C:cytoplasm; IEA.
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0009374; F:biotin binding; IEA.
GO; GO:0004086; F:carbamoyl-phosphate synthase activity; IEA.
GO; GO:0016874; F:ligase activity; IEA.
GO; GO:0004736; F:pyruvate carboxylase activity; IEA.
GO; GO:0006094; P:gluconeogenesis; IEA.
GO; GO:0008152; P:metabolism; IEA.
InterPro; IPR001892; Biotin_BS.
InterPro; IPR005482; Biotin_carb_C.
InterPro; IPR000089; Biotin_lipoYL.
InterPro; IPR005483; CPase_L_D2.
InterPro; IPR005479; CPase_L_D2.
InterPro; IPR005481; CPase_L_N.
InterPro; IPR000891; HMGL-like.
InterPro; IPR003379; PYC_OADA.
InterPro; IPR005930; Pyruv_carbox.
Pfam; PF02785; Biotin_carb_C; 1.
Pfam; PF00364; biotin_lipoYL; 1.
Pfam; PF00289; CPase_L_chain; 1.
Pfam; PF02786; CPase_L_D2; 1.
Pfam; PF00682; HMGL-like; 1.
Pfam; PF02436; PYC_OADA; 1.
PRINTS; PR00098; CPASE.
TIGRfams; TIGR01235; pyruv_carbox; 1.
PROSITE; PS00188; BIOTIN; 1.
PROSITE; PS00866; CPASE_1; 1.
PROSITE; PS00867; CPASE_2; 1.
Complete proteome.
SEQUENCE 1144 AA; 127709 MW; 519FA29A8008F326 CRC64;

Query Match 27.6%; Score 170; DB 16; Length 1144;
Best Local Similarity 47.3%; Pred. No. 2e-05;
Matches 35; Conservative 13; Mismatches 26; Indels 0; Gaps 0;

QY 48 AGKAGEGEIPAPLAGTYSKILVKEGDTVKAGQTVLVLEAMKQETEINAPTDGKVKVLVK 107
Db 1070 ADSSNKKEIGASIPGNVVVFVPGDKVKKGDLSLMVIEAMKQETNVSVSEDTVGIGFVK 1129
QY 108 ERDAVQGGGLIKI 121
Db 1130 EGDQVQSGQLLVKL 1143

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Search completed: March 3, 2004, 10:31:09
Job time : 48.1146 secs

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OM protein - protein search, using sw model

Run on: March 3, 2004, 10:24:54 ; Search time 7.29167 Seconds
(without alignments)
499.873 Million cell updates/sec

Title: US-09-987-485A-2
Perfect score: 342
Sequence: 1 BGEIPAPLAGTVSKILVKEG.....KVLVKERDAVQGGGLIKIG 70

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	342	100.0	123	1	BCCP_PROFR
2	173	50.6	567	1	PYCB_METJA
3	165	48.2	595	1	DCOA_KLEPN
4	152	44.4	590	1	DCOA_SALTY
5	148	43.3	717	1	MCCA_MOUSE
6	145	42.4	130	1	BCCP_SPMU
7	143	41.8	70	1	BCCP_LYCES
8	143	41.8	725	1	MCCA_HUMAN
9	143	41.8	734	1	MCCA_ARATH
10	140	40.9	568	1	PYCB_METH
11	138.5	40.5	157	1	BCCP_PORPU
12	138	40.4	1180	1	PYC2_YEAST
13	133	38.9	1178	1	PYC1_YEAST
14	132	38.6	1189	1	PYC_PICPA
15	130	38.0	598	1	BCCA_MYCLE
16	130	38.0	731	1	MCCA_SOYBN
17	129	37.7	1178	1	PYC_MOUSE
18	126.5	37.0	181	1	BCCP_ANASP
19	124.5	36.4	654	1	BCCA_MYCTU
20	122	35.7	164	1	BCCP_CHLTR
21	121	35.4	1178	1	PYC_HUMAN
22	119	34.8	1178	1	PYC_RAT
23	118	34.5	70	1	BTB7_MYCSM
24	118	34.5	163	1	BCCP_CHLMU
25	115.5	33.8	547	1	ODP2_PSEAE
26	115	33.6	70	1	BTB7_MYCTU
27	114	33.3	438	1	ODP2_MYCCA
28	113.5	33.2	629	1	ODP2_ECOLI
29	111	32.5	704	1	PCCA_RAT
30	110	32.2	703	1	PCCA_HUMAN
31	108.5	31.7	167	1	BCCP_CHLPN
32	108	31.6	553	1	ODO2_MYCTU
33	107	31.3	70	1	BTB7_MYCLE

34	104	30.4	1835	1	DURL_YEAST	P32528	saccharomyc
35	103.5	30.3	567	1	ODP2_HAEIN	P45118	haemophilus
36	103	30.1	462	1	ODPB_ZYMMO	O66113	zymomonas m
37	102.5	30.0	155	1	BCCP_HAEIN	P43874	haemophilus
38	102	29.8	544	1	ODP2_ACHLA	P35489	acholeplasm
39	102	29.8	637	1	ODP2_AZOVI	P10802	azotobacter
40	101.5	29.7	262	1	BCCP_SOYBN	Q42783	glycine max
41	98.5	28.8	156	1	BCCP_PSEAE	P37799	pseudomonas
42	97.5	28.5	156	1	BCCP_ECOLI	P02905	escherichia
43	97	28.4	384	1	ODP2_MYCGE	P47514	mycoplasma
44	95	27.8	463	1	ODO2_YEAST	P19262	saccharomyc
45	94.5	27.6	152	1	BCCP_CYACA	O19918	cyanidium c

ALIGNMENTS

RESULT 1
BCCP_PROFR
ID BCCP_PROFR STANDARD; PRT; 123 AA.
AC P02904;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Biotin carboxyl carrier protein of methylmalonyl-CoA carboxyl-
transferase (Transcarboxylase, 1.3S subunit).
OS Propionibacterium freudenreichii shermanii.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Propionibacterineae; Propionibacteriaceae; Propionibacterium.
OX NCBI_TaxID=1752;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85298212; PubMed=3898065;
RA Murtif V.L., Bahler C.R., Samols D.;
RT "Cloning and expression of the 1.3S biotin-containing subunit of
transcarboxylase.";
RL Proc. Natl. Acad. Sci. U.S.A. 82:5617-5621(1985).
RN [2]
RP SEQUENCE.
RX MEDLINE=80049796; PubMed=40985;
RA Maloy W.L., Bowien B.U., Zwolinski G.K., Kumar G.K., Wood H.G.,
RA Ericsson L.H., Walsh K.A.;
RT "Amino acid sequence of the biotinyl subunit from transcarboxylase.";
RL J. Biol. Chem. 254:11615-11622(1979) ✓
RN [3]
RP MUTAGENESIS OF ALA-87; MET-88; LYS-89 AND MET-90.
RX MEDLINE=92406744; PubMed=1526981;
RA Shenoy B.C., Xie Y., Park V.L., Kumar G.K., Beegen H., Wood H.G.,
RA Samols D.;
RT "The importance of methionine residues for the catalysis of the
biotin enzyme, transcarboxylase. Analysis by site-directed
mutagenesis.";
RL J. Biol. Chem. 267:18407-18412(1992).
RN [4]
RP STRUCTURE BY NMR.
RX MEDLINE=98066416; PubMed=9398186;
RA Reddy D.V., Shenoy B.C., Carey P.R., Soennichsen F.D.;
RT "Absence of observable biotin-protein interactions in the 1.3S
subunit of transcarboxylase: an NMR study.";
RL Biochemistry 36:14676-14682(1997).
CC -!- FUNCTION: THE BIOTINYL 1.3S SUBUNIT SERVES AS A CARBOXYL CARRIER
CC BETWEEN THE SUBSTRATE BINDING SITES ON THE 12S AND 5S SUBUNITS.
CC -!- SUBUNIT: TRANSCARBOXYLASE IS COMPOSED OF THREE SUBUNITS: 1.3S,
CC 5S, AND 12S. THE CORE OF THE ENZYME IS COMPOSED OF SIX 12S
CC SUBUNITS. ON EACH SIDE OF THE CORE THERE ARE THREE PAIRS OF 5S
CC SUBUNITS. EACH 5S DIMER IS ATTACHED TO THE CORE BY TWO 1.3S
CC SUBUNITS. THUS THE TOTAL NUMBER OF CHAINS IS 30 (6 + 12 + 12).
CC -----
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CC -----

DR EMBL; M11738; AAA25674.1; --
DR PIR; A03401; BKIP.
DR PDB; 1DCZ; 10-MAY-00.
DR PDB; 1DD2; 24-MAR-00.
DR PDB; 1O78; 21-NOV-02.
DR InterPro; IPR001882; Biotin_BS.
DR InterPro; IPR000089; Biotin_lipoyl.
DR Pfam; PF00364; biotin_lipoyl; 1.
DR PROSITE; PS00188; BIOTIN; 1.
KW Biotin; 3D-structure.
FT BINDING 89 BIOTIN.
SQ SEQUENCE 123 AA; 12367 MW; D0980C2065EA9A89 CRC64;

Query Match 100.0%; Score 342; DB 1; Length 123;
Best Local Similarity 100.0%; Pred. No. 2.2e-26;
Matches 70; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGEIPAPLAGTGVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTQKVEKVLVKERDAV 60
DB 54 EGEIPAPLAGTGVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTQKVEKVLVKERDAV 113

QY 61 QGGQGLIKIG 70
DB 114 QGGQGLIKIG 123

RESULT 2

PYCB_METJA STANDARD; PRT; 567 AA.
AC Q58628;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Pyruvate carboxylase subunit B (EC 6.4.1.1) (Pyruvic carboxylase B).
GN PYCB OR MJ1231.
OS Methanococcus jannaschii.
OC Archaea; Euryarchaeota; Methanococci; Methanococcales;
OC Methanocaldococcaceae; Methanocaldococcus.
OX NCBI_TaxID=2190;
RN [1]_

SEQUENCE FROM N.A.
STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
RX MEDLINE=96337999; PubMed=8688087;
RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
RA Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,
RA Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
RA Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
RA Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
RT "Complete genome sequence of the methanogenic archaeon, Methanococcus
jannaschii.";
RL Science 273:1058-1073(1996).
RN [2]

SEQUENCE OF 190-125; 260-270; 277-289; 277-289; 309-325; 328-358;
RP 370-380; 386-409; 422-438; 491-506 AND 491-506, AND FUNCTION.
RX MEDLINE=21034791; PubMed=11195096;
RA Mukhopadhyay B., Patel V.J., Wolfe R.S.;
RT "A stable archaeal pyruvate carboxylase from the hyperthermophile
Methanococcus jannaschii.";
RL Arch. Microbiol. 174:406-414(2000).

CC -!- FUNCTION: Pyruvate carboxylase catalyzes a 2-step reaction,
CC involving the ATP-dependent carboxylation of the covalently
CC attached biotin in the first step and the transfer of the carboxyl
CC group to pyruvate in the second.

CC -!- CATALYTIC ACTIVITY: ATP + pyruvate + HCO(3)(-) = ADP + phosphate +
CC oxaloacetate.

CC -!- COFACTOR: ATP, magnesium (or manganese or cobalt), pyruvate and
CC bicarbonate.

CC -!- ENZYME REGULATION: INHIBITED BY MAGNESIUM, WHEN ITS CONCENTRATION
CC EXCEEDED THE ATP ONE, AND BY HIGH CONCENTRATION OF ATP AND ALPHA-
CC KETOGLUTARATE.

CC -!- PATHWAY: Gluconeogenesis.
CC -!- SUBUNIT: Heterooctamer of four A and four B subunits.

CC -!- MASS SPECTROMETRY: MW=64160; METHOD=MALDI.

CC -!- MISCELLANEOUS: ITS OPTIMUM PH IS 8.5 AND THE OPTIMUM TEMPERATURE

CC IS 80-90 DEGREES CELSIUS.

CC -!- SIMILARITY: WITH OTHER BIOTIN CARBOXYLASES, LIPOAMIDE TRANSFERASES
CC AND CARBAMYL PHOSPHATE SYNTHETASES.

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CC -----

DR EMBL; U67563; AAB99233.1; --

DR PIR; F64453; F64453.

DR HSSP; P02905; 1A6X.

DR TIGR; MJ1231; --

DR InterPro; IPR001882; Biotin_BS.

DR InterPro; IPR000089; Biotin_lipoyl.

DR InterPro; IPR000891; HMGL-like.

DR InterPro; IPR005776; Oada.

DR InterPro; IPR003379; PYC_OADA.

DR Pfam; PF00364; biotin_lipoyl; 1.

DR Pfam; PF00682; HMGL-like; 1.

DR Pfam; PF02436; PYC_OADA; 1.

DR TIGRFAMs; TIGR01108; oada; 1.

DR PROSITE; PS00188; BIOTIN; 1.

KW Ligase; Multifunctional enzyme; Gluconeogenesis; Magnesium; Pyruvate;

KW Biotin; Complete proteome.

FT BINDING 52 60 PYRUVATE (BY SIMILARITY).

FT BINDING 533 533 BIOTIN (BY SIMILARITY).

SQ SEQUENCE 567 AA; 63907 MW; 5E07800622545628 CRC64;

Query Match 50.6%; Score 173; DB 1; Length 567;

Best Local Similarity 50.7%; Pred. No. 1.8e-09;

Matches 35; Conservative 12; Mismatches 22; Indels 0; Gaps 0;

QY 1 EGEIPAPLAGTGVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTQKVEKVLVKERDAV 60

DB 498 EGAVTSPFRGMVTIKVKEGDKVKGDVIVVLEAMKMEHPESPVEGTVERILIDEGDAV 557

QY 61 QGGQGLIKI 69

DB 558 NVGDVIMII 566

RESULT 3

DCOA_KLEPN

ID DCOA_KLEPN STANDARD; PRT; 595 AA.

AC P13187;

DT 01-JAN-1990 (Rel. 13, Created)

DT 01-JAN-1990 (Rel. 13, Last sequence update)

DT 01-JUL-1993 (Rel. 26, Last annotation update)

DE Oxaloacetate decarboxylase alpha chain (EC 4.1.1.3).

GN OADA.

OS Klebsiella pneumoniae.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;

OC Enterobacteriaceae; Klebsiella.

OX NCBI_TaxID=573;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=88257085; PubMed=2454915;

RA Schwarz E., Oesterheld D., Reinke H., Beyreuther K., Dimroth P.;

RT "The sodium ion translocating oxalacetate decarboxylase of Klebsiella

RT pneumoniae. Sequence of the biotin-containing alpha-subunit and

RT relationship to other biotin-containing enzymes.";

RL J. Biol. Chem. 263:9640-9645(1988).

```
CC -!- FUNCTION: Lyase and sodium transporter.
CC -!- CATALYTIC ACTIVITY: Oxaloacetate = pyruvate + CO(2).
CC -!- COFACTOR: Biotin and requires a sodium ion.
CC -!- SUBUNIT: Composed of three chains (alpha, beta, and gamma).
CC -----
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CC -----
CC EMBL; J03885; AAA25120.1; -.
CC PIR; A28088; A28088.
CC HSSP; P02905; 1A6X.
CC InterPro; IPR001882; Biotin_BS.
CC InterPro; IPR000089; Biotin_lipoyl.
CC InterPro; IPR000891; HMGL-like.
CC InterPro; IPR005776; Oada.
CC InterPro; IPR003379; PYC_OADA.
CC Pfam; PF00364; biotin_lipoyl; 1.
CC Pfam; PF00682; HMGL-like; 1.
CC Pfam; PF02436; PYC_OADA; 1.
CC TIGRFAMs; TIGR01108; oada; 1.
CC PROSITE; PS00188; BIOTIN; 1.
KW Decarboxylase; Lyase; Sodium transport; Biotin.
FT INIT MET 0
FT BINDING 561 561 BIOTIN (BY SIMILARITY).
SQ SEQUENCE 595 AA; 63402 MW; AA744A95A6E9488C CRC64;

Query Match 48.2%; Score 165; DB 1; Length 595;
Best Local Similarity 53.0%; Pred. No. 1.le-08;
Matches 35; Conservative 9; Mismatches 22; Indels 0; Gaps 0;

QY 4 IPAPLAGTVSKILVKEGDTVKGQTVLVLEAMKMETEINAPTDGKVKVLVKERDAVQGG 63
Db 529 VTAPLAGTIWKVLASEGQTVAAAGEVLLILEAMKMETEIRAAQAGTVRGIAVKAGDAVAVG 588

QY 64 QGLIKI 69
Db 589 DTLMTL 594

RESULT 4
DCOA_SALTY STANDARD; PRT; 590 AA.
AC Q03030;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Oxaloacetate decarboxylase alpha chain (EC 4.1.1.3).
GN (OADA1 OR OADA OR STM0055) AND (OADA2 OR STM3352).
OS Salmonella typhimurium.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_TaxID=602;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=LT2;
RX MEDLINE=93054591; PubMed=1331067;
RA Woehlke G., Wifling K., Dimroth P.;
RT "Sequence of the sodium ion pump oxaloacetate decarboxylase from
RT Salmonella typhimurium."
RL J. Biol. Chem. 267:22798-22803(1992).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=LT2 / SGSC1412 / ATCC 700720;
RX MEDLINE=21534948; PubMed=11677609;
RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
RA Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
RA Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
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RA Waterston R., Wilson R.K.;
RT "Complete genome sequence of Salmonella enterica serovar Typhimurium
RT LT2."
RL Nature 413:852-856(2001).
CC -!- FUNCTION: Lyase and sodium transporter.
CC -!- CATALYTIC ACTIVITY: Oxaloacetate = pyruvate + CO(2).
CC -!- COFACTOR: Biotin and requires a sodium ion.
CC -!- SUBUNIT: Composed of three chains (alpha, beta, and gamma).
CC -----
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CC -----
CC EMBL; M96434; AAA02973.1; -.
CC PIR; A28088; A28088.
CC HSSP; P02905; 1A6X.
CC StyGene; SG10259; oada1.
CC StyGene; SG???; oada2.
CC InterPro; IPR001882; Biotin_BS.
CC InterPro; IPR000089; Biotin_lipoyl.
CC InterPro; IPR000891; HMGL-like.
CC InterPro; IPR005776; Oada.
CC InterPro; IPR003379; PYC_OADA.
CC Pfam; PF00364; biotin_lipoyl; 1.
CC Pfam; PF00682; HMGL-like; 1.
CC TIGRFAMs; TIGR01108; oada; 1.
CC PROSITE; PS00188; BIOTIN; 1.
KW Decarboxylase; Lyase; Sodium transport; Biotin; Complete proteome.
FT INIT MET 0
FT BINDING 556 556 BIOTIN (BY SIMILARITY).
SQ SEQUENCE 590 AA; 63075 MW; 4EA421F9324AFD7B CRC64;

Query Match 44.4%; Score 152; DB 1; Length 590;
Best Local Similarity 48.5%; Pred. No. 2e-07;
Matches 32; Conservative 9; Mismatches 25; Indels 0; Gaps 0;

QY 4 IPAPLAGTVSKILVKEGDTVKGQTVLVLEAMKMETEINAPTDGKVKVLVKERDAVQGG 63
Db 524 VTAPLAGTIWKVIATEGQTVAEQDVLLILEAMKMETEIRAAQAGTVRGIAVKSGDAVSVG 583

QY 64 QGLIKI 69
Db 584 DTLMTL 589

RESULT 5
MCCA_MOUSE STANDARD; PRT; 717 AA.
AC Q99MR8; Q9D8R2;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Methylcrotonyl-CoA carboxylase alpha chain, mitochondrial precursor
DE (EC 6.4.1.4) (3-Methylcrotonyl-CoA carboxylase 1) (MCCase alpha
DE subunit) (3-methylcrotonyl-CoA:carbon dioxide ligase alpha subunit).
GN MCCC1 OR MCCA.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=21102410; PubMed=11181649;
RA Baumgartner M.R., Almashanu S., Suomalala T., Obie C., Cole R.N.,
RA Packman S., Baumgartner E.R., Valle D.;
```

RT "The molecular basis of human 3-methylcrotonyl-CoA carboxylase
RT deficiency.";
RL J. Clin. Invest. 107:495-504 (2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Pancreas;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690 (2001).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
CC -!- CATALYTIC ACTIVITY: ATP + 3-methylcrotonyl-CoA + HCO(3)(-) = ADP +
CC phosphate + 3-methylglutaconyl-CoA.
CC -!- COFACTOR: Biotin.
CC -!- PATHWAY: Leucine catabolism.
CC -!- SUBUNIT: Probably a dodecamer composed of six biotin-containing
CC alpha subunits and six beta subunits.
CC -!- SUBCELLULAR LOCATION: Mitochondrial matrix (By similarity).
CC -----
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CC -----
CC EMBL; AF310338; AAG50244.1; -;
CC EMBL; AK007782; BAB25253.1; -;
CC EMBL; BC021382; AAH21382.1; -;
CC HSSP; P24182; 1DVI.
CC MGD; MGI:1919289; Mccc1.
CC GO; GO:0005759; C:mitochondrial matrix; ISS.

DR GO; GO:0009374; F:biotin binding; ISS.
DR GO; GO:0004485; F:methylcrotonyl-CoA carboxylase activity; ISS.
DR GO; GO:0006768; P:biotin metabolism; ISS.
DR GO; GO:0006552; P:leucine catabolism; ISS.
DR InterPro; IPR001882; Biotin_BS.
DR InterPro; IPR005482; Biotin_carb_C.
DR InterPro; IPR000089; Biotin_lipoyl.
DR InterPro; IPR005479; CPase_L_D2.
DR InterPro; IPR005481; CPase_L_N.
DR Pfam; PF02785; Biotin_carb_C; 1.
DR Pfam; PF00364; biotin_lipoyl; 1.
DR Pfam; PF00289; CPSase_L_chain; 1.
DR Pfam; PF02786; CPSase_L_D2; 1.
DR PROSITE; PS00188; BIOTIN; 1.
DR PROSITE; PS00867; CPSASE_2; 1.
KW Mitochondrion; Ligase; Biotin; ATP-binding; Transit peptide.
FT TRANSIT 1 44 MITOCHONDRION (POTENTIAL).
FT CHAIN 45 717 METHYLCROTONYL-COA CARBOXYLASE ALPHA
FT CHAIN 45 717 CHAIN.
FT NP_BIND 205 210 ATP (POTENTIAL).
FT ACT_SITE 335 335 BY SIMILARITY.
FT BINDING 677 677 BIOTIN (BY SIMILARITY).
FT DOMAIN 709 714 POLY-GLU.
FT CONFLICT 324 324 R -> K (IN REF. 3).
FT CONFLICT 507 507 A -> P (IN REF. 1).
SQ SEQUENCE 717 AA; 79343 MW; F653FE7AC1E5AA90 CRC64;

Query Match 43.3%; Score 148; DB 1; Length 717;

Best Local Similarity 50.0%; Pred. No. 5.8e-07;

Matches 28; Conservative 11; Mismatches 17; Indels 0; Gaps 0;

QY 1 EGEIPAPLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTQGVKVLVKE 56

Db 642 QGGTIAPMTGTIEKVFVKAGDRVKAGDSLMVMIAMKMEHTIKAPKDGRIKKVFFSE 697

RESULT 6

BCCP_STRMU

ID BCCP_STRMU STANDARD; PRT; 130 AA.

AC P29337;

DT 01-DEC-1992 (Rel. 24, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Biotin carboxyl carrier protein (BCCP).

GN BCC OR SMU.1016.

OS Streptococcus mutans.

OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;

OC Streptococcus.

OX NCBI_TaxID=1309;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=UT-041 / Serotype C;

RX MEDLINE=93159778; PubMed=8431283;

RA Wang D., Wayne M.M., Taricani M., Buckingham K., Sandham H.J.;

RT "Biotin-containing protein as a cause of false positive clones in

RT gene probing with streptavidin/biotin.";

RL Biotechniques 14:209-212 (1993).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=UA159 / ATCC 700610 / Serotype C;

RX MEDLINE=22295063; PubMed=12397186;

RA Ajdic D., McShan W.M., McLaughlin R.E., Savic G., Chang J.,

RA Carson M.B., Primeaux C., Tian R., Kenton S., Jia H., Lin S., Qian Y.,

RA Li S., Zhu H., Najjar F., Lai H., White J., Roe B.A., Ferretti J.J.;

RT "Genome sequence of Streptococcus mutans UA159, a cariogenic dental

RT pathogen.";

RL Proc. Natl. Acad. Sci. U.S.A. 99:14434-14439 (2002).

CC -----

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RT "NEDO human cDNA sequencing project.";
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal muscle;
RX MEDLINE=2238257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -|- CATALYTIC ACTIVITY: ATP + 3-methylcrotonyl-CoA + ADP +
phosphate + 3-methylglutaconyl-CoA.
CC -|- COFACTOR: Biotin.
CC -|- PATHWAY: Leucine catabolism.
CC -|- SUBUNIT: Probably a dodecamer composed of six biotin-containing
alpha subunits and six beta subunits.
CC -|- SUBCELLULAR LOCATION: Mitochondrial matrix.
CC -|- DISEASE: Defects in MCCC1 are the cause of 3-
methylcrotonylglycinuria type I (MCGI) [MIM:210200]; also
designated CGA or CG2. MCGI is a recessive disease that is
characterized by muscular hypotonia and atrophy, probably of
spinal origin.
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or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF310972; AAG53095.1; -
DR EMBL; AB029826; BAA99407.1; -
DR EMBL; AF297332; AAK67986.1; -
DR EMBL; AF310339; AAG50245.1; -
DR EMBL; AK023051; BAB14377.1; -
DR EMBL; BC004214; AAH04214.1; -
DR EMBL; BC004187; AAH04187.1; -
DR Genew; HGNC:6936; MCCC1.
DR GK; Q96RQ3; -
DR MIM; 210200; -
DR GO; GO:0005759; C:mitochondrial matrix; NAS.
DR GO; GO:0009374; F:biotin binding; NAS.
DR GO; GO:0004485; F:methylcrotonyl-CoA carboxylase activity; NAS.
DR GO; GO:0006768; P:biotin metabolism; NAS.
DR GO; GO:0006552; P:leucine catabolism; NAS.
DR InterPro; IPR001882; Biotin_BS.
DR InterPro; IPR005482; Biotin_carb_C.
DR InterPro; IPR000089; Biotin_lipoyL.
DR InterPro; IPR005479; CPase_L_D2.
DR InterPro; IPR005481; CPase_L_N.
DR Pfam; PF02785; Biotin_carb_C; 1.
DR Pfam; PF00364; biotin_lipoyL; 1.
DR Pfam; PF00289; CPase_L_chain; 1.
DR Pfam; PF02786; CPase_L_D2; 1.
DR PROSITE; PS00188; BIOTIN; 1.
DR PROSITE; PS00867; CPASE_2; 1.

KW Mitochondrion; Ligase; Biotin; ATP-binding; Transit peptide;
KW Disease mutation; Polymorphism.
FT TRANSIT 1 47 MITOCHONDRION (POTENTIAL).
FT CHAIN 48 725 METHYLCROTONYL-COA CARBOXYLASE ALPHA
CHAIN.
FT NP BIND 209 214 ATP (POTENTIAL).
FT ACT_SITE 339 339 BY SIMILARITY.
FT BINDING 681 681 BIOTIN (BY SIMILARITY).
FT DOMAIN 538 541 POLY-SER.
FT DOMAIN 713 718 POLY-GLU.
FT VARIANT 289 289 A -> V (in MCGI; mild form).
FT VARIANT 325 325 /FTid=VAR_012785.
FT VARIANT 385 385 M -> R (in MCGI).
FT VARIANT 385 385 /FTid=VAR_012786.
FT VARIANT 437 437 R -> S (in MCGI; severe form).
FT VARIANT 437 437 /FTid=VAR_012787.
FT VARIANT 464 464 L -> P (in MCGI; severe form).
FT VARIANT 464 464 /FTid=VAR_012788.
FT VARIANT 532 532 P -> H.
FT VARIANT 532 532 /FTid=VAR_012789.
FT VARIANT 535 535 D -> H (in MCGI; severe form).
FT VARIANT 535 535 /FTid=VAR_012790.
FT CONFLICT 469 469 S -> F (in MCGI; asymptomatic form).
FT SEQUENCE 725 AA; 80433 MW; B847C6B80606B6C0 CRC64;
Query Match 41.8%; Score 143; DB 1; Length 725;
Best Local Similarity 52.9%; Pred. No. 1.8e-06;
Matches 27; Conservative 10; Mismatches 14; Indels 0; Gaps 0;
QY 6 APLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTQGVKVLVKE 56
DB 651 APMTGTIEKVFVKAGDKVKAGDSLMVMIAMKMEHTIKSPKDGTVKKVFYRE 701
RESULT 9
MCCA_ARATH STANDARD; PRT; 734 AA.
ID MCCA_ARATH
AC Q42523; Q9SA61;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Methylcrotonyl-CoA carboxylase alpha chain, mitochondrial precursor
DE (EC 6.4.1.4) (3-Methylcrotonyl-CoA carboxylase 1) (MCCase alpha
subunit) (3-methylcrotonyl-CoA:carbon dioxide ligase alpha subunit).
DE MCCA OR AT1G03090 OR F1003_8 OR F1003_9.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RC STRAIN=cv. Columbia;
RX MEDLINE=95232183; PubMed=7716229;
RA Weaver L.M., Lebrun L., Franklin A., Huang L., Hoffman N.,
RA Wurtele E.S., Nikolau B.J.;
RT "Molecular cloning of the biotinylated subunit of 3-methylcrotonyl-
coenzyme A carboxylase of Arabidopsis thaliana.";
RL Plant Physiol. 107:1013-1014(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=21016719; PubMed=11130712;
RA Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,
RA White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,
RA Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,
RA Dunn P., Etgu P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y.,
RA Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,
RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
RA Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,


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RT "Purification, regulation, and molecular and biochemical
RT characterization of pyruvate carboxylase from Methanobacterium
RT thermoautotrophicum strain deltaH."
RL J. Biol. Chem. 273:5155-5166(1998).
CC -!- FUNCTION: PYRUVATE CARBOXYLASE CATALYZES A 2-STEP REACTION,
CC INVOLVING THE ATP-DEPENDENT CARBOXYLATION OF THE COVALENTLY
CC ATTACHED BIOTIN IN THE FIRST STEP AND THE TRANSFER OF THE CARBOXYL
CC GROUP TO PYRUVATE IN THE SECOND. THE MAXIMUM ACTIVITY IS AT PH 8
CC AND 60 DEGREES CELSIUS.
CC -!- CATALYTIC ACTIVITY: ATP + pyruvate + HCO(3) (-) = ADP + phosphate +
CC oxaloacetate.
CC -!- COFACTOR: ATP, magnesium (or manganese or cobalt), pyruvate and
CC bicarbonate.
CC -!- ENZYME REGULATION: INHIBITED BY ADP AND ALPHA-KETOGLUTARATE.
CC -!- SUBUNIT: Heterooctamer of four A and four B subunits.
CC -!- SIMILARITY: WITH OTHER BIOTIN CARBOXYLASES, LIPOAMIDE TRANSFERASES
CC AND CARBAMYL PHOSPHATE SYNTHETASES.
CC -----
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CC -----
DR EMBL; AE000881; AAB85596.1; -.
DR EMBL; AF039105; AAC12719.1; -.
DR PIR; C69014; C69014.
DR HSSP; P02905; 1BDO.
DR InterPro; IPR001882; Biotin_BS.
DR InterPro; IPR000089; Biotin_lipoyl.
DR InterPro; IPR000891; HMGL-like.
DR InterPro; IPR005776; Oada.
DR InterPro; IPR003379; PYC OADA.
DR Pfam; PF00364; biotin_lipoyl; 1.
DR Pfam; PF00682; HMGL-like; 1.
DR Pfam; PF02436; PYC OADA; 1.
DR TIGRFAMS; TIGR01108; oada; 1.
DR PROSITE; PS00188; BIOTIN; FALSE NEG.
KW Ligase; Multifunctional enzyme; Gluconeogenesis; Magnesium; Pyruvate;
KW Biotin; Complete proteome.
FT BINDING 54 69 PYRUVATE.
FT BINDING 534 534 BIOTIN.
FT SEQUENCE 568 AA; 63955 MW; D328715AB0328DBB CRC64;

Query Match 40.9%; Score 140; DB 1; Length 568;
Best Local Similarity 43.5%; Pred. No. 2.7e-06;
Matches 30; Conservative 11; Mismatches 28; Indels 0; Gaps 0;

QY 1 EGEIPAPLAGTVSKILVKEGDTVKGQTVLVLEAMKMETEINAPTGDGKVEKVLKRDVAV 60
Db 499 EGAVKSTMQGMVVKLKVSQDQVAGDVAVVVEAMKMEINDIQTPHGGVVVEKIYTAEGKV 558
QY 61 QGGQGLIKI 69
Db 559 ETGDIIMVI 567

RESULT 11
BCCP_PORPU STANDARD; PRT; 157 AA.
ID BCCP_PORPU
AC P51283;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Biotin carboxyl carrier protein of acetyl-CoA carboxylase (BCCP).
GN ACCB.
OS Porphyra purpurea.
OG Chloroplast.
OC Eukaryota; Rhodophyta; Bangiophyceae; Bangiales; Bangiaceae; Porphyra.
OX NCBI_TaxID=2787;
RA [1]
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```
RP SEQUENCE FROM N.A.
RC STRAIN=Avonport;
RA Reith M.E., Munnolland J.;
RT "Complete nucleotide sequence of the Porphyra purpurea chloroplast
RT genome."
RL Plant Mol. Biol. Rep. 13:333-335(1995).
CC -!- FUNCTION: This protein is a component of the acetyl coenzyme A
CC carboxylase complex; first, biotin carboxylase catalyzes the
CC carboxylation of the carrier protein and then the transcarboxylase
CC transfers the carboxyl group to form malonyl-CoA.
CC -!- PATHWAY: Long-chain fatty acid biosynthesis; first step.
CC -!- SUBCELLULAR LOCATION: Chloroplast.
CC -----
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CC -----
DR EMBL; U38804; AAC08169.1; -.
DR PIR; S73204; S73204.
DR HSSP; P02905; 1BDO.
DR InterPro; IPR001249; AcCoA_biotinCC.
DR InterPro; IPR001882; Biotin_BS.
DR InterPro; IPR000089; Biotin_lipoyl.
DR Pfam; PF00364; biotin_lipoyl; 1.
DR PRINTS; PR01071; ACOABIOTINCC.
DR TIGRFAMS; TIGR00531; BCCP; 1.
DR PROSITE; PS00188; BIOTIN; 1.
KW Fatty acid biosynthesis; Biotin; Chloroplast.
FT BINDING 122 122 BIOTIN (BY SIMILARITY).
FT SEQUENCE 157 AA; 17519 MW; 5CFF079B2410E777 CRC64;

Query Match 40.5%; Score 138.5; DB 1; Length 157;
Best Local Similarity 42.5%; Pred. No. 1.2e-06;
Matches 31; Conservative 12; Mismatches 23; Indels 7; Gaps 1;

QY 4 IPAPLAGTV-----SKILVKEGDTVKGQTVLVLEAMKMETEINAPTGDGKVEKVLVKE 56
Db 83 IVSPMVGTFFYHSPAPGEKIFVQGVGDIVKCNQTVCIIEAMKLMNEIEAIEGIIILVKN 142
QY 57 RDAVQGGQGLIKI 69
Db 143 GDIVDCGQALMKV 155

RESULT 12
PYC2 YEAST STANDARD; PRT; 1180 AA.
ID PYC2 YEAST
AC P32327;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Pyruvate carboxylase 2 (EC 6.4.1.1) (pyruvic carboxylase 2) (PCB 2).
GN PYC2 OR YBR218C OR YBR1507.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
RX MEDLINE=92017667; PubMed=1921979;
RA Stucka R., Dequin S., Salmon J.-M., Gancedo C.;
RT "DNA sequences in chromosomes II and VII code for pyruvate
RT carboxylase isoenzymes in Saccharomyces cerevisiae: analysis of
RT pyruvate carboxylase-deficient strains."
RL Mol. Gen. Genet. 229:307-315(1991).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C;
RA Dubois E., el Bakkoury M., Glansdorff N., Messenguy F., Pierard A.,
```

CC EMBL; J03889; AAA34843.1; -
DR EMBL; Z72584; CAA96765.1; -
DR PIR; S64066; QYBYP.
DR HSSP; P24182; 1BNC.
DR GermOnline; 141110; -
DR SGD; S0003030; PYC1.
DR GO; GO:0005829; C:cytosol; IDA.
DR GO; GO:0004736; F:pyruvate carboxylase activity; IDA.
DR InterPro; IPR001882; Biotin_BS.
DR InterPro; IPR005482; Biotin_carb_C.
DR InterPro; IPR000089; Biotin_lipoyl.
DR InterPro; IPR005479; CPase_L_D2.
DR InterPro; IPR005481; CPase_L_N.
DR InterPro; IPR000891; HMGL-like.
DR InterPro; IPR003379; PYC_OADA.
DR InterPro; IPR005930; Pyruv_carbox.
DR Pfam; PF02785; Biotin_carb_C; 1.
DR Pfam; PF00364; biotin_lipoyl; 1.
DR Pfam; PF00289; CPSase_L_chain; 1.
DR Pfam; PF02786; CPSase_L_D2; 1.
DR Pfam; PF00682; HMGL-like; 1.
DR Pfam; PF02436; PYC_OADA; 1.
DR TIGRFAMs; TIGR01235; pyruv_carbox; 1.
DR PROSITE; PS00188; BIOTIN; 1.
DR PROSITE; PS00866; CPSASE_1; 1.
DR PROSITE; PS00867; CPSASE_2; 1.
KW Ligase; Multifunctional enzyme; Biotin; Gluconeogenesis; ATP-binding;
KW Zinc; Multigene family.
FT NP_BIND 182 187 ATP (POTENTIAL).
FT ACT_SITE 312 312 BY SIMILARITY.
FT BINDING 1135 1135 BIOTIN (BY SIMILARITY).
FT CONFLICT 462 462 T -> G (IN REF. 1).
FT CONFLICT 493 493 V -> D (IN REF. 1).
FT CONFLICT 595 595 R -> A (IN REF. 1).
FT CONFLICT 619 619 E -> Q (IN REF. 1).
FT CONFLICT 664 664 G -> S (IN REF. 1).
FT CONFLICT 772 772 A -> R (IN REF. 1).
FT CONFLICT 879 879 E -> Q (IN REF. 1).
FT CONFLICT 909 909 Q -> K (IN REF. 1).
SQ SEQUENCE 1178 AA; 130099 MW; BC7110A8AFB23E04 CRC64;

Query Match 38.9%; Score 133; DB 1; Length 1178;
Best Local Similarity 42.2%; Pred. No. 2.6e-05;
Matches 27; Conservative 15; Mismatches 22; Indels 0; Gaps 0;

QY 4 IPAPLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVLVKERDAVQGG 63
Db 1103 IGAPMAGVIVEVKHKGSLIKKGQPPAVLSAMKMEMIISPSDGGQVKEVFDGENVDSS 1162

QY 64 QGLI 67
Db 1163 DLLV 1166

RESULT 14
ID PYC_PICPA STANDARD; PRT; 1189 AA.
AC P78992;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Pyruvate carboxylase (EC 6.4.1.1) (Pyruvic carboxylase) (PCB).
GN PYC1.
OS Pichia pastoris (Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Pichia.
OX NCBI_TaxID=4922;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98301182; PubMed=9639311;
RA Menendez J., Delgado J., Gancedo C.;
RT "Isolation of the Pichia pastoris PYC1 gene encoding pyruvate

carboxylase and identification of a suppressor of the pyc
phenotype.";
Yeast 14:647-654(1998).
-!- FUNCTION: Pyruvate carboxylase catalyzes a 2-step reaction,
involving the ATP-dependent carboxylation of the covalently
attached biotin in the first step and the transfer of the
carboxyl group to pyruvate in the second (By similarity).
-!- CATALYTIC ACTIVITY: ATP + pyruvate + HCO(3) (-) = ADP + phosphate +
oxaloacetate.
-!- COFACTOR: Biotin and zinc.
-!- PATHWAY: Gluconeogenesis.
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SIMILARITY: WITH OTHER BIOTIN CARBOXYLASES, LIPOAMIDE TRANSFERASES
AND CARBAMYL PHOSPHATE SYNTHETASES.

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CC EMBL; Y11106; CAA71993.1; -
DR HSSP; P24182; 1DV1.
DR InterPro; IPR001882; Biotin_BS.
DR InterPro; IPR005482; Biotin_carb_C.
DR InterPro; IPR000089; Biotin_lipoyl.
DR InterPro; IPR005483; CPase_L.
DR InterPro; IPR005479; CPase_L_D2.
DR InterPro; IPR005481; CPase_L_N.
DR InterPro; IPR000891; HMGL-like.
DR InterPro; IPR003379; PYC_OADA.
DR InterPro; IPR005930; Pyruv_carbox.
DR Pfam; PF02785; Biotin_carb_C; 1.
DR Pfam; PF00364; biotin_lipoyl; 1.
DR Pfam; PF00289; CPSase_L_chain; 1.
DR Pfam; PF02786; CPSase_L_D2; 1.
DR Pfam; PF00682; HMGL-like; 1.
DR Pfam; PF02436; PYC_OADA; 1.
DR PRINTS; PR00098; CPSASE.
DR TIGRFAMs; TIGR01235; pyruv_carbox; 1.
DR PROSITE; PS00188; BIOTIN; 1.
DR PROSITE; PS00866; CPSASE_1; 1.
DR PROSITE; PS00867; CPSASE_2; 1.
KW Ligase; Multifunctional enzyme; Biotin; Gluconeogenesis; ATP-binding;
KW Zinc.
FT NP_BIND 185 190 ATP (POTENTIAL).
FT ACT_SITE 315 315 BY SIMILARITY.
FT BINDING 1140 1140 BIOTIN (BY SIMILARITY).
SQ SEQUENCE 1189 AA; 131400 MW; 8B6E858079657914 CRC64;

Query Match 38.6%; Score 132; DB 1; Length 1189;
Best Local Similarity 46.6%; Pred. No. 3.2e-05;
Matches 27; Conservative 11; Mismatches 20; Indels 0; Gaps 0;

QY 3 EIPAPLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVLVKERDAV 60
Db 1107 EIGAPMAGVVEVRVHENGVEVKKGDFIAVLSAMKMEMVISSPVAGRIGIAVKENDSV 1164

RESULT 15
ID BCCA_MYCLE STANDARD; PRT; 598 AA.
AC P46392;
DT 01-NOV-1995 (Rel. 32, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Acetyl-/propionyl-coenzyme A carboxylase alpha chain [Includes: Biotin
carboxylase (EC 6.3.4.14); Biotin carboxyl carrier protein (BCCP)].
GN BCCA OR ML0726 OR B1308_C1_129.
OS Mycobacterium leprae.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;


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DR Pfam; PF00364; biotin_lipoyl; 1.
DR Pfam; PF00289; Cpsase_L_chain; 1.
DR Pfam; PF02786; Cpsase_L_D2; 1.
DR PROSITE; PS00188; BIOTIN; 1.
DR PROSITE; PS00866; CPSASE; 1; 1.
DR PROSITE; PS00867; CPSASE_2; 1.
KW Mitochondrion; Ligase; Biotin; ATP-binding; Transit peptide.
FT TRANSIT 1 22 MITOCHONDRION.
FT CHAIN 23 731 METHYL-CROTONYL-COA CARBOXYLASE ALPHA CHAIN.
FT NP_BIND 193 198 ATP (POTENTIAL).
FT ACT_SITE 324 324 BY SIMILARITY.
FT BINDING 695 695 BIOTIN (BY SIMILARITY).
FT CONFLICT 68 68 R -> K (IN REF. 1; AAA53141).
FT CONFLICT 75 75 T -> S (IN REF. 1; AAA53141).
FT CONFLICT 78 78 E -> K (IN REF. 1; AAA53141).
SQ SEQUENCE 731 AA; 80619 MW; C4D5A94F8123A9B4 CRC64;

Query Match 38.0%; Score 130; DB 1; Length 731;
Best Local Similarity 42.0%; Pred. No. 3.2e-05;
Matches 29; Conservative 12; Mismatches 28; Indels 0; Gaps 0;

QY 1 EGEIPAPLAGTVSKILVKEGDTVKGQTVLVLEAMKMETEINAPTDGKVEKVLVKERDAV 60
Db 660 QGTWAPMAGLVVKLVENKTRVEEGQPVVLVLEAMKMEHVVKAPSSGYVHGLQLMVGEQV 719
QY 61 QGGQGLIKI 69
Db 720 SDGSVLFVS 728

RESULT 17
PYC_MOUSE
ID PYC_MOUSE STANDARD; PRT; 1178 AA.
AC Q05920;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Pyruvate carboxylase, mitochondrial precursor (EC 6.4.1.1) (Pyruvic
DE carboxylase) (PCB).
GN PC OR PCX.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Adipocyte;
RX MEDLINE=93189578; PubMed=8446588;
RA Zhang J., Xia W.L., Brew K., Ahmad F.;
RT "Adipose pyruvate carboxylase: amino acid sequence and domain
RT structure deduced from cDNA sequencing."
RL Proc. Natl. Acad. Sci. U.S.A. 90:1766-1770(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Liver;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettner M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
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RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC !- FUNCTION: Pyruvate carboxylase catalyzes a 2-step reaction,
CC involving the ATP-dependent carboxylation of the covalently
CC attached biotin in the first step and the transfer of the
CC carboxyl group to pyruvate in the second. Catalyzes in a tissue
CC specific manner, the initial reactions of glucose (liver, kidney)
CC and lipid (adipose tissue, liver, brain) synthesis from pyruvate.
CC !- CATALYTIC ACTIVITY: ATP + pyruvate + HCO(3)(-) = ADP + phosphate +
CC oxaloacetate.
CC !- COFACTOR: Biotin and manganese.
CC !- PATHWAY: Gluconeogenesis and lipogenesis.
CC !- SUBUNIT: Homotetramer.
CC !- SUBCELLULAR LOCATION: Mitochondrial matrix.
CC !- TISSUE SPECIFICITY: Liver, kidney, adipose tissue, liver and
CC brain.
CC !- SIMILARITY: WITH OTHER BIOTIN CARBOXYLASES, LIPOAMIDE TRANSFERASES
CC AND CARBAMYL PHOSPHATE SYNTHETASES.
CC -----
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CC -----
DR EMBL; L09192; AAA39737.1; -.
DR EMBL; BC055030; AAH55030.1; -.
DR PIR; A47255; A47255.
DR HSSP; P24182; 1BNC.
DR SWISS-2DPAGE; Q05920; MOUSE.
DR MGD; MGI:97520; PCX.
DR InterPro; IPR001882; Biotin_BS.
DR InterPro; IPR005482; Biotin_carb_C.
DR InterPro; IPR000089; Biotin_lipoyl.
DR InterPro; IPR005479; CPase_L_D2.
DR InterPro; IPR005481; CPase_L_N.
DR InterPro; IPR000891; HMGL-like.
DR InterPro; IPR003379; PYC_OADA.
DR InterPro; IPR005930; Pyruv_carbox.
DR Pfam; PF02785; Biotin_carb_C; 1.
DR Pfam; PF00364; biotin_lipoyl; 1.
DR Pfam; PF00289; Cpsase_L_chain; 1.
DR Pfam; PF02786; Cpsase_L_D2; 1.
DR Pfam; PF00682; HMGL-like; 1.
DR Pfam; PF02436; PYC_OADA; 1.
DR TIGRFAMS; TIGR01235; pyruv_carbox; 1.
DR PROSITE; PS00188; BIOTIN; 1.
KW Ligase; Multifunctional enzyme; Biotin; Manganese; Gluconeogenesis;
KW ATP-binding; Mitochondrion; Lipid synthesis; Transit peptide.
FT TRANSIT 1 20 MITOCHONDRION (POTENTIAL).
FT CHAIN 21 1178 PYRUVATE CARBOXYLASE.
FT DOMAIN 21 549 BIOTIN CARBOXYLASE (BY SIMILARITY).
FT DOMAIN 550 1000 CARBOXYLTRANSFERASE (BY SIMILARITY).
FT DOMAIN 1096 1178 BIOTIN CARBOXYL CARRIER PROTEIN
FT NP_BIND 198 203 ATP (BY SIMILARITY).
FT ACT_SITE 328 328 BY SIMILARITY.
FT BINDING 1144 1144 BIOTIN (BY SIMILARITY).
SQ SEQUENCE 1178 AA; 129684 MW; 14CEA0F9DA8B8127 CRC64;

Query Match 37.7%; Score 129; DB 1; Length 1178;
Best Local Similarity 40.6%; Pred. No. 6.2e-05;
Matches 28; Conservative 14; Mismatches 27; Indels 0; Gaps 0;

QY 1 EGEIPAPLAGTVSKILVKEGDTVKGQTVLVLEAMKMETEINAPTDGKVEKVLVKERDAV 60
Db 1109 KGQIGAPMPGKVIDIKVAAGDKVAKGQPLCVLSAMKMETVTSPEGTIRKVHTKMTL 1168
QY 61 QGGQGLIKI 69
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CC -|- COFACTOR: Biotin.
CC -|- PATHWAY: Long-chain fatty acid biosynthesis; first step.
CC -|- SUBUNIT: MULTIMER COMPRISED OF 2 DIFFERENT SUBUNITS, THE LARGER
CC ONE (63/64 kDa) HAS BIOTIN CARBOXYLASE AND BIOTIN CARRIER
CC FUNCTIONS, WHILE THE SMALLER SUBUNIT POSSESSES CARBOXYLTRANSFERASE
CC AND SUBSTRATE BINDING ACTIVITY.
CC -|- SIMILARITY: TO OTHER BIOTIN-DEPENDENT ENZYMES AND CARBAMOYL-
CC PHOSPHATE SYNTHETASES.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; Z19549; CAA79609.1; -.
CC EMBL; Z95556; CAB08919.1; -.
CC EMBL; AE007094; AAK46880.1; -.
CC EMBL; BX248342; CAD97390.1; -.
CC PIR; B55579; B55579.
CC HSSP; P24182; IBNC.
CC TIGR; MT2576; -.
CC TubercuList; RV2501c; -.
CC InterPro; IPR001882; Biotin_BS.
CC InterPro; IPR005482; Biotin_carb_C.
CC InterPro; IPR000089; Biotin_lipoyl.
CC InterPro; IPR005479; CPase_L_D2.
CC InterPro; IPR005481; CPase_L_N.
CC Pfam; PF02785; Biotin_carb_C; 1.
CC Pfam; PF00364; biotin_lipoyl; 1.
CC Pfam; PF00289; CPase_L_chain; 1.
CC Pfam; PF02786; CPase_L_D2; 1.
CC PROSITE; PS00188; BIOTIN; 1.
CC PROSITE; PS00866; CPASE_1; 1.
CC PROSITE; PS00867; CPASE_2; 1.
CC Fatty acid biosynthesis; Ligase; Biotin; Multifunctional enzyme;
KW ATP-binding; Complete proteome.
KW DOMAIN 1 437 BIOTIN CARBOXYLASE.
FT NP BIND 588 654 BIOTIN CARBOXYL CARRIER PROTEIN.
FT ACT SITE 294 294 ATP (BY SIMILARITY).
FT BINDING 620 620 BY SIMILARITY.
FT SEQUENCE 654 AA; 70592 MW; FAA0A1A46432CABF CRC64;

Query Match 36.4%; Score 124.5; DB 1; Length 654;
Best Local Similarity 41.8%; Pred. No. 9.8e-05;
Matches 28; Conservative 14; Mismatches 24; Indels 1; Gaps 1;

QY 3 EIPAPLAGTVSKILVKEGDTVKGQTVLVLEAMKMETEINAPTDGKVEKVLVKERDAVQG 62
Db 587 EWSPMPGVSIVAVQVESGSQISAGDVVVVVVEAMKMEHSLEAPVSGRVQ-VLVSVGDQVKV 645

QY 63 GQGLIKI 69
Db 646 EQVLARI 652

RESULT 20
BCCP_CHLTR STANDARD; PRT; 164 AA.
AC 084125;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Biotin carboxyl carrier protein of acetyl-CoA carboxylase (BCCP).
GN ACCB OR CT123.
OS Chlamydia trachomatis.
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxID=813;
RN [1]
RP SEQUENCE FROM N.A.
```

```
RC STRAIN=D/UW-3/Cx;
RX MEDLINE=99000809; PubMed=9784136;
RA Stephens R.S., Kalman S., Lammel C.J., Fan J., Marathe R., Aravind L.,
RA Mitchell W.P., Olinger L., Tatusov R.L., Zhao Q., Koonin E.V.,
RA Davis R.W.;
RT "Genome sequence of an obligate intracellular pathogen of humans:
RT Chlamydia trachomatis.";
RL Science 282:754-759(1998).
CC -|- FUNCTION: This protein is a component of the acetyl coenzyme A
CC carboxylase complex; first, biotin carboxylase catalyzes the
CC carboxylation of the carrier protein and then the transcarboxylase
CC transfers the carboxyl group to form malonyl-CoA (By similarity).
CC -|- PATHWAY: Long-chain fatty acid biosynthesis; first step.
CC -|- SUBUNIT: Homodimer (By similarity).
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AE001286; AAC67714.1; -.
CC PIR; G71553; G71553.
CC HSSP; P02905; 3BDO.
CC PHCI-2DPAGE; O84125; -.
CC InterPro; IPR001249; ACCoA_biotinCC.
CC InterPro; IPR001882; Biotin_BS.
CC InterPro; IPR000089; Biotin_lipoyl.
CC Pfam; PF00364; biotin_lipoyl; 1.
CC PRINTS; PR01071; ACOABIOTINCC.
CC TIGRFAMS; TIGR00531; BCCP; 1.
CC PROSITE; PS00188; BIOTIN; 1.
CC Fatty acid biosynthesis; Biotin; Complete proteome.
KW BINDING 128 128 BIOTIN (BY SIMILARITY).
FT SEQUENCE 164 AA; 18198 MW; BD0BA4CEBC2D384C CRC64;

Query Match 35.7%; Score 122; DB 1; Length 164;
Best Local Similarity 36.1%; Pred. No. 4.7e-05;
Matches 30; Conservative 11; Mismatches 28; Indels 14; Gaps 2;

QY 1 EGEIPA-----PLAGTV-----SKILVKEGDTVKGQTVLVLEAMKMETEINAPTD 46
Db 79 ESEAPAQGDFFIVSPLVGTFGSPSPAPAFIKPGDVTSEDVTVCIVAMKVMNEVKAGMS 138

QY 47 GKVEKVLVKERDAVQGGGLIKI 69
Db 139 GRVEILLITNGDPVQFGSKLFRI 161

RESULT 21
PYC_HUMAN STANDARD; PRT; 1178 AA.
AC P11498; Q16705;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Pyruvate carboxylase, mitochondrial precursor (EC 6.4.1.1) (Pyruvic
DE carboxylase) (PCB).
GN PC.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney, and Liver;
RX MEDLINE=95002202; PubMed=7918683;
RA Wexler I.D., Du Y., Lisgaris M.V., Mandal S.K., Freytag S.O.,
RA Yang B.-S., Liu T.-C., Kwon M., Patel M.S., Kerr D.S.;
RT "Primary amino acid sequence and structure of human pyruvate
RT carboxylase.";
```


RL Biochim. Biophys. Acta 1227:46-52 (1994).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=94324922; PubMed=8048912;
RA Mackay N., Rigat B., Douglas C., Chen H.S., Robinson B.H.;
RT "cDNA cloning of human kidney pyruvate carboxylase.";
RL Biochem. Biophys. Res. Commun. 202:1009-1014 (1994).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney, and Liver;
RA Walker M.E., Jitrapakdee S., Val D.L., Wallace J.C.;
RL Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=22389257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Maruina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [5]
RP SEQUENCE OF 1083-1178 FROM N.A.
RX MEDLINE=87212051; PubMed=3555348;
RA Lamhonwah A.-M., Quan F., Gravel R.A.;
RT "Sequence homology around the biotin-binding site of human propionyl-
CoA carboxylase and pyruvate carboxylase.";
RL Arch. Biochem. Biophys. 254:631-636 (1987).
RN [6]
RP SEQUENCE OF 1135-1178 FROM N.A.
RX MEDLINE=85030380; PubMed=6548474;
RA Freytag S.O., Collier K.J.;
RT "Molecular cloning of a cDNA for human pyruvate carboxylase.
Structural relationship to other biotin-containing carboxylases and
regulation of mRNA content in differentiating preadipocytes.";
RL J. Biol. Chem. 259:12831-12837 (1984).
RN [7]
RP VARIANTS PC DEFICIENCY THR-610 AND ILE-743.
RX MEDLINE=98254451; PubMed=9585612;
RA Carbone M.A., MacKay N., Ling M., Cole D.E.C., Douglas C., Rigat B.,
RA Feigenbaum A., Clarke J.T.R., Haworth J.C., Greenberg C.R.,
RA Seargeant L., Robinson B.H.;
RT "Amerindian pyruvate carboxylase deficiency is associated with two
distinct missense mutations.";
RL Am. J. Hum. Genet. 62:1312-1319 (1998).
RN [8]
RP VARIANTS PC DEFICIENCY ALA-145 AND CYS-451.
RX MEDLINE=98244401; PubMed=9585002;
RA Wexler I.D., Kerr D.S., Du Y., Kaung M.M., Stephenson W., Lusk M.M.,
RA Wappner R.S., Higgins J.J.;
RT "Molecular characterization of pyruvate carboxylase deficiency in two
consanguineous families.";
RL Pediatr. Res. 43:579-584 (1998).
CC -!- FUNCTION: Pyruvate carboxylase catalyzes a 2-step reaction,
involving the ATP-dependent carboxylation of the covalently
attached biotin in the first step and the transfer of the
carboxyl group to pyruvate in the second. Catalyzes in a tissue

specific manner, the initial reactions of glucose (liver, kidney)
and lipid (adipose tissue, liver, brain) synthesis from pyruvate.
CC -!- CATALYTIC ACTIVITY: ATP + pyruvate + HCO(3) (-) = ADP + phosphate +
oxaloacetate.
CC -!- COFACTOR: Biotin and manganese.
CC -!- PATHWAY: Gluconeogenesis and lipogenesis.
CC -!- SUBUNIT: Homotetramer.
CC -!- SUBCELLULAR LOCATION: Mitochondrial matrix.
CC -!- DISEASE: Defects in PC are the cause of pyruvate carboxylase
deficiency (PC deficiency) [MIM:266150]. PC deficiency leads to
lactic acidosis, mental retardation and death. It occurs in three
forms: mild or type A, severe neonatal or type B, and a very mild
lacticacidemia.
CC -!- SIMILARITY: WITH OTHER BIOTIN CARBOXYLASES, LIPOAMIDE TRANSFERASES
AND CARBAMYL PHOSPHATE SYNTHETASES.
CC
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CC
CC EMBL; U04641; AAA99537.1; -.
CC EMBL; S72370; AAB31500.1; -.
CC EMBL; U30891; AAA82937.1; -.
CC EMBL; BC011617; AAH11617.1; -.
CC EMBL; M26122; AAA36423.1; -.
CC EMBL; K02282; AAA60033.1; -.
CC PIR; G01933; JC2460.
CC HSSP; P24182; 1BNC.
CC Genew; HGNC:8636; PC.
CC GK; P11498; -.
CC MIM; 266150; -.
CC GO; GO:0005524; F:ATP binding; TAS.
CC GO; GO:0009374; F:biotin binding; TAS.
CC GO; GO:0004736; F:pyruvate carboxylase activity; TAS.
CC InterPro; IPR001882; Biotin_BS.
CC InterPro; IPR005482; Biotin_carb_C.
CC InterPro; IPR000089; Biotin_lipoyl.
CC InterPro; IPR005479; CPase_L_D2.
CC InterPro; IPR005481; CPase_L_N.
CC InterPro; IPR000891; HMGL-like.
CC InterPro; IPR003379; PYC_OADA.
CC InterPro; IPR005930; Pyruv_carbox.
CC Pfam; PF02785; Biotin_carb_C; 1.
CC Pfam; PF00364; biotin_lipoyl; 1.
CC Pfam; PF00289; CPase_L_chain; 1.
CC Pfam; PF02786; CPase_L_D2; 1.
CC Pfam; PF00682; HMGL-like; 1.
CC Pfam; PF02436; PYC_OADA; 1.
CC TIGRFAMs; TIGR01235; pyruv_carbox; 1.
CC PROSITE; PS00188; BIOTIN; 1.
KW Ligase; Multifunctional enzyme; Biotin; Manganese; Gluconeogenesis;
KW ATP-binding; Mitochondrion; Lipid synthesis; Transit peptide;
KW Disease mutation.
FT TRANSIT 1 20 MITOCHONDRION (POTENTIAL).
FT CHAIN 21 1178 PYRUVATE CARBOXYLASE.
FT DOMAIN 21 549 BIOTIN CARBOXYLASE (BY SIMILARITY).
FT DOMAIN 550 1000 CARBOXYLTRANSFERASE (BY SIMILARITY).
FT DOMAIN 1096 1178 BIOTIN CARBOXYL CARRIER PROTEIN
(BY SIMILARITY).
FT NP_BIND 198 203 ATP (BY SIMILARITY).
FT ACT_SITE 328 328 BY SIMILARITY.
FT BINDING 1144 1144 BIOTIN (BY SIMILARITY).
FT VARIANT 145 145 V -> A (in PC deficiency; mild).
FT VARIANT 451 451 /FTId=VAR_015199.
FT VARIANT 451 451 R -> C (in PC deficiency; mild).
FT VARIANT 610 610 /FTId=VAR_015200.
FT VARIANT 610 610 A -> T (in PC deficiency; mild).
FT VARIANT 743 743 /FTId=VAR_008095.
FT VARIANT 743 743 M -> I (in PC deficiency; mild).

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FT CONFLICT 225 226 /FTID=VAR 008096;
FT CONFLICT 352 352 LA -> WP (IN REF. 2).
FT CONFLICT 385 386 A -> S (IN REF. 3).
FT CONFLICT 486 487 RS -> PT (IN REF. 2).
FT CONFLICT 638 638 EL -> DV (IN REF. 2).
FT CONFLICT 729 729 P -> R (IN REF. 2).
FT CONFLICT 774 775 E -> A (IN REF. 2).
FT CONFLICT 1178 1178 DT -> AP (IN REF. 2).
SQ SEQUENCE 1178 AA; 129633 MW; 381F527553A20095 CRC64;

Query Match 35.4%; Score 121; DB 1; Length 1178;
Best Local Similarity 40.6%; Pred. No. 0.00037;
Matches 28; Conservative 13; Mismatches 28; Indels 0; Gaps 0;

QY 1 EGEIPAPLAGTVSKILVKEGDTVKGQTVLVLEAMKMETEINAPTQKVEKVLVKERDAV 60
Db 1109 KGQIGAPMPGKVIDIKVAGAKVAKGQPLCVLSAMKMETVVTSPMEGTIRKVVHTKDMTL 1168
QY 61 QGGQGLIKI 69
Db 1169 EGDDLILEI 1177

RESULT 22
PVC_RAT STANDARD; PRT; 1178 AA.
ID PVC_RAT STANDARD; PRT; 1178 AA.
AC PS2873; Q64555; PRT; 1178 AA.
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Pyruvate carboxylase, mitochondrial precursor (EC 6.4.1.1) (Pyruvic
DE carboxylase) (PCB).
GN PC.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=96096548; PubMed=8522203;
RA Lehn D.A., Moran S.M., Macdonald M.J.;
RT "The sequence of the rat pyruvate carboxylase-encoding cDNA.";
RL Gene 165:331-332(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Wistar; TISSUE=Liver;
RX MEDLINE=96257760; PubMed=8687410;
RA Jitrapakdee S., Booker G.W., Cassidy A.I., Wallace J.C.;
RT "Cloning, sequencing and expression of rat liver pyruvate
RT carboxylase.";
RL Biochem. J. 316:631-637(1996).
CC -!- FUNCTION: Pyruvate carboxylase catalyzes a 2-step reaction,
CC involving the ATP-dependent carboxylation of the covalently
CC attached biotin in the first step and the transfer of the carboxyl
CC group to pyruvate in the second. Catalyzes in a tissue specific
CC manner, the initial reactions of glucose (liver, kidney) and lipid
CC (adipose tissue, liver, brain) synthesis from pyruvate.
CC -!- CATALYTIC ACTIVITY: ATP + pyruvate + HCO(3)(-) = ADP + phosphate +
CC oxaloacetate.
CC -!- COFACTOR: Biotin and manganese (By similarity).
CC -!- PATHWAY: Gluconeogenesis and lipogenesis.
CC -!- SUBUNIT: Homotetramer (By similarity).
CC -!- SUBCELLULAR LOCATION: Mitochondrial matrix.
CC -!- SIMILARITY: WITH OTHER BIOTIN CARBOXYLASES, LIPOAMIDE TRANSFERASES
CC AND CARBAMYL PHOSPHATE SYNTHETASES.
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CC -----
DR EMBL; U32314; AAA96256.1; -.
DR EMBL; U36585; AAC52668.1; -.
DR PIR; S68252; JC4391.
DR HSSP; P24182; IBNC.
DR InterPro; IPR001882; Biotin_BS.
DR InterPro; IPR005482; Biotin_carb_C.
DR InterPro; IPR000089; Biotin_lipoyl.
DR InterPro; IPR005479; CPase_L_D2.
DR InterPro; IPR005481; CPase_L_N.
DR InterPro; IPR000891; HMGL-Like.
DR InterPro; IPR003379; PYC_OADA.
DR InterPro; IPR005930; Pyruv_carbox.
DR Pfam; PF02785; Biotin_carb_C; 1.
DR Pfam; PF00364; biotin_lipoyl; 1.
DR Pfam; PF00289; CPSase_L_chain; 1.
DR Pfam; PF02786; CPSase_L_D2; 1.
DR Pfam; PF00682; HMGL-Like; 1.
DR Pfam; PF02436; PYC_OADA; 1.
DR TIGRFAMs; TIGR01235; Pyruv_carbox; 1.
DR PROSITE; PS00188; BIOTIN; 1.
KW Ligase; Multifunctional enzyme; Biotin; Manganese; Gluconeogenesis;
KW ATP-binding; Mitochondrion; Lipid synthesis; Transit peptide.
FT TRANSIT 1 20 MITOCHONDRION (POTENTIAL).
FT CHAIN 21 1178 PYRUVATE CARBOXYLASE.
FT DOMAIN 21 549 BIOTIN CARBOXYLASE (BY SIMILARITY).
FT DOMAIN 550 1000 CARBOXYLTRANSFERASE (BY SIMILARITY).
FT DOMAIN 1096 1178 BIOTIN CARBOXYL CARRIER PROTEIN
FT (BY SIMILARITY).
FT NP_BIND 198 203 ATP (BY SIMILARITY).
FT ACT_SITE 328 328 BY SIMILARITY.
FT BINDING 1144 1144 BIOTIN (BY SIMILARITY).
FT CONFLICT 222 222 P -> S (IN REF. 2).
FT CONFLICT 866 866 D -> I (IN REF. 2).
FT CONFLICT 977 977 G -> R (IN REF. 2).
SQ SEQUENCE 1178 AA; 129689 MW; 8E5FA19BC132A8DD CRC64;

Query Match 34.8%; Score 119; DB 1; Length 1178;
Best Local Similarity 37.7%; Pred. No. 0.00057;
Matches 26; Conservative 15; Mismatches 28; Indels 0; Gaps 0;

QY 1 EGEIPAPLAGTVSKILVKEGDTVKGQTVLVLEAMKMETEINAPTQKVEKVLVKERDAV 60
Db 1109 KGQIGAPMPGKVIDIKVAGAKVAKGQPLCVLSAMKMETVVTSPMEGTIRKVVHTKDMTL 1168
QY 61 QGGQGLIKI 69
Db 1169 EGDDLILEI 1177

RESULT 23
BTB7_MYCSM STANDARD; PRT; 70 AA.
ID BTB7_MYCSM STANDARD; PRT; 70 AA.
AC Q9XCD6;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Biotinylated protein TB7.3 homolog.
OS Mycobacterium smegmatis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1772;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 70084 / mc(2)155;
RX MEDLINE=99328972; PubMed=10400584;
RA Fernandes N.D., Wu Q.-L., Kong D., Puyang X., Garg S., Husson R.N.;
RT "A mycobacterial extracytoplasmic sigma factor involved in survival
RT following heat shock and oxidative stress.";
RL J. Bacteriol. 181:4266-4274(1999).
CC -----
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CC -----

DR EMBL; AF144091; AAD41812.1; --
DR HSSP; P10802; 1IYU.
DR InterPro; IPR001882; Biotin_BS.
DR InterPro; IPR000089; Biotin_lipoyl.
DR Pfam; PF00364; biotin_lipoyl; 1.
DR PROSITE; PS00188; BIOTIN; FALSE_NEG.
KW Biotin.
FT INIT MET 0 0 BY SIMILARITY.
FT BINDING 36 36 BIOTIN (BY SIMILARITY).
SQ SEQUENCE 70 AA; 7306 MW; 975C293B63C770C8 CRC64;

Query Match 34.5%; Score 118; DB 1; Length 70;
Best Local Similarity 39.3%; Pred. No. 5.1e-05;
Matches 24; Conservative 14; Mismatches 23; Indels 0; Gaps 0;

QY 3 EIPAPLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVLVKERDAVQG 62
Db 3 DVRAEIVASVLEVVVHEGDTGEGDTLVLESKMEIPVLAEVAGTVTKVNVABGDVIA 62

QY 63 G 63
Db 63 G 63

RESULT 24

BCCP_CHLMU STANDARD; PRT; 163 AA.
AC Q9PKR5;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Biotin carboxyl carrier protein of acetyl-CoA carboxylase (BCCP).
GN ACCB OR TC0399.
OS Chlamydia muridarum.
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxID=83560;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MoPn / Nigg;
RX MEDLINE=20150255; PubMed=10684935;
RA Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
RA White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S.,
RA Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,
RA Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.,
RA Eisen J., Fraser C.M.;
RT "Genome sequences of Chlamydia trachomatis MoPn and Chlamydia
RL pneumoniae AR39.";
RL Nucleic Acids Res. 28:1397-1406(2000).
CC -!- FUNCTION: This protein is a component of the acetyl coenzyme A
CC carboxylase complex; first, biotin carboxylase catalyzes the
CC carboxylation of the carrier protein and then the transcarboxylase
CC transfers the carboxyl group to form malonyl-CoA (By similarity).
CC -!- PATHWAY: long-chain fatty acid biosynthesis; first step.
CC -!- SUBUNIT: Homodimer (By similarity).
CC -----
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CC -----
CC EMBL; AE002306; AAF39256.1; --
DR PIR; C81708; C81708.
DR HSSP; P02905; 1BDO.

DR TIGR; TC0399; --
DR InterPro; IPR001249; AcCoA_biotinCC.
DR InterPro; IPR001882; Biotin_BS.
DR InterPro; IPR000089; Biotin_lipoyl.
DR Pfam; PF00364; biotin_lipoyl; 1.
DR PRINTS; PR01071; ACOABIOTINCC.
DR TIGRFAMs; TIGR00531; BCCP; 1.
DR PROSITE; PS00188; BIOTIN; 1.
KW Fatty acid biosynthesis; Biotin; Complete proteome.
FT BINDING 127 127 BIOTIN (BY SIMILARITY).
SQ SEQUENCE 163 AA; 18084 MW; 8536D58B5CE11D3B CRC64;

Query Match 34.5%; Score 118; DB 1; Length 163;
Best Local Similarity 40.3%; Pred. No. 0.00011;
Matches 31; Conservative 10; Mismatches 28; Indels 8; Gaps 2;

QY 1 EGE-IPAPLAGTV-----SKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKV 52
Db 84 EGDIVSPLVGTFTYCAPSPESPAFVKPGDIVSBDTVVCIVEAMKVMNEVKAGMAGRVEEV 143
QY 53 LVKERDAVQGGGLIKI 69
Db 144 LITNGDPVQFGSKLPRI 160

RESULT 25

ODP2_PSEAE STANDARD; PRT; 547 AA.
AC Q59638;
DT 01-NOV-1997 (Rel. 35, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Dihydrolipoamide acetyltransferase component of pyruvate dehydrogenase
DE complex (EC 2.3.1.12) (E2).
GN ACEF OR ACEB OR PA5016.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PAO;
RX MEDLINE=97315227; PubMed=9171401;
RA Rae J.L., Cutfield J.F., Lamont I.L.;
RT "Sequences and expression of pyruvate dehydrogenase genes from
RL Pseudomonas aeruginosa.";
RL J. Bacteriol. 179:3561-3571(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 15692 / PAO1;
RX MEDLINE=20437337; PubMed=10984043;
RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warren P.,
RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
RA Garber R.L., Goltry L., Tolentino E., Westbrook-Wadman S., Yuan Y.,
RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Reizer J., Sailer M.H., Hancock R.E.W., Lory S., Olson M.V.;
RT "Complete genome sequence of Pseudomonas aeruginosa PAO1, an
RT opportunistic pathogen.";
RL Nature 406:959-964(2000).
CC -!- FUNCTION: The pyruvate dehydrogenase complex catalyzes the overall
CC conversion of pyruvate to acetyl-CoA and CO(2). It contains
CC multiple copies of three enzymatic components: pyruvate
CC dehydrogenase (E1), dihydrolipoamide acetyltransferase (E2) and
CC lipoamide dehydrogenase (E3).
CC -!- CATALYTIC ACTIVITY: Acetyl-CoA + dihydrolipoamide = CoA + S-
CC acetyldihydrolipoamide.
CC -!- COFACTOR: Contains 2 covalently bound lipoyl cofactors (By
CC similarity).
CC -!- SUBUNIT: Forms a 24-polypeptide structural core with octahedral
CC symmetry.
CC -!- SIMILARITY: Belongs to the 2-oxoacid dehydrogenase family.
CC -!- SIMILARITY: Contains 2 lipoyl-binding domains.

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EMBL; U47920; AAC45354.1; -;
EMBL; AE004914; AAG08401.1; -;
PIR; H83018; H83018.
HSSP; P10802; IEAF.
InterPro; IPR001078; 2Oxoacid_dh.
InterPro; IPR006256; AceF.
InterPro; IPR000089; Biotin_lipoyl.
InterPro; IPR004167; E3_binding.
InterPro; IPR003016; Lipoyl_BS.
Pfam; PF00198; 2-oxoacid_dh; 1.
Pfam; PF00364; biotin_lipoyl; 2.
Pfam; PF02817; e3_binding; 1.
ProDom; PD001115; 2Oxoacid_dh; 1.
TIGRFAMs; TIGR01348; PDHac_trf_long; 1.
PROSITE; PS00189; LIPOYL; 2.
Glycolysis; Transferase; Acyltransferase; Repeat; Lipoyl;
KW Complete proteome.
KW BINDING 41 LIPOYL (BY SIMILARITY).
FT BINDING 159 159 LIPOYL (BY SIMILARITY).
FT ACT SITE 520 520 POTENTIAL.
FT CONFLICT 225 225 A -> V (IN REF. 1).
FT CONFLICT 295 301 GGAGATG -> AVPAPR (IN REF. 1).
FT CONFLICT 328 329 MQ -> IE (IN REF. 1).
SQ SEQUENCE 547 AA; 56709 MW; 24EI5CC9A590CB4 CRC64;

Query Match 33.8%; Score 115.5; DB 1; Length 547;
Best Local Similarity 37.5%; Pred. No. 0.00061;
Matches 27; Conservative 14; Mismatches 26; Indels 5; Gaps 1;

QY 3 EIPAPLAGTVSK-----ILVKEGDTVKAGQTVLVLEAMKMETEINAPTGGKVEKVLVKER 57
Db 121 DIKVPDIGSAGKANVIEVMVKAGDTVEADQSLITLES DKASMEIPSPASGVVESVIKVG 180

QY 58 DAVQGGQGLIKI 69
Db 181 DEVGTGDLILKL 192

RESULT 26
BTB7 MYCTU STANDARD; PRT; 70 AA.
ID BTB7 MYCTU STANDARD; PRT; 70 AA.
AC O05845;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Biotinylated protein TB7.3.
GN RV3221C OR MT3317 OR MTCY07D11.05 OR MB3247C.
OS Mycobacterium tuberculosis, and
OS Mycobacterium bovis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1773, 1765;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=M.tuberculosis; STRAIN=H37RV;
RX MEDLINE=98295987; PubMed=9634230;
RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D., Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekai F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S., Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Taylor K., Whitehead S., Barrell B.G.; Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;

RT "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence."
RL Nature 393:537-544(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=M.tuberculosis; STRAIN=CDC 1551 / Oshkosh;
RX MEDLINE=22206494; PubMed=12218036;
RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O., Peterson J., DeBoy R., Dodson R., Gwinn M., Haft D., Hickey E., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg S.L., Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A., Bishai W., Jacobs W.R. Jr., Venter J.C., Fraser C.M.;
RT "Whole-genome comparison of Mycobacterium tuberculosis clinical and laboratory strains."
RL J. Bacteriol. 184:5479-5490(2002).
RN [3]
RP SEQUENCE OF 1-15, AND BIOTINYLATION.
RC SPECIES=M.tuberculosis;
RX MEDLINE=20072687; PubMed=10603390;
RA Skjot R.L., Oettinger T., Rosenkrands I., Ravn P., Brock I., Jacobsen S., Andersen P.;
RT "Comparative evaluation of low-molecular-mass proteins from Mycobacterium tuberculosis identifies members of the ESAT-6 family as immunodominant T-cell antigens."
RL Infect. Immun. 68:214-220(2000).
RN [4]
RP SEQUENCE FROM N.A.
RC SPECIES=M.bovis; STRAIN=AF2122/97;
RX MEDLINE=22709107; PubMed=12788972;
RA Garnier T., Eiglmeier K., Camus J.-C., Medina N., Mansoor H., Pryor M., Duthoy S., Grondin S., Lacroix C., Monsemp C., Simon S., Harris B., Atkin R., Doggett J., Mayes R., Keating L., Wheeler P.R., Parkhill J., Barrell B.G., Cole S.T., Gordon S.V., Hewinson R.G.;
RT "The complete genome sequence of Mycobacterium bovis."
RL Proc. Natl. Acad. Sci. U.S.A. 100:7877-7882(2003).
CC -----
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CC -----
EMBL; Z95120; CAB08316.1; -;
EMBL; AE007143; AAK47659.1; ALT_INIT.
EMBL; BX248345; CAD95339.1; -;
PIR; F70596; F70596.
HSSP; P10802; ILYU.
TIGR; MT3317; -;
TuberculList; RV3221C; -;
InterPro; IPR001882; Biotin_BS.
InterPro; IPR000089; Biotin_lipoyl.
Pfam; PF00364; biotin_lipoyl; 1.
PROSITE; PS00188; BIOTIN; FALSE_NEG.
KW Biotin; Antigen; Complete proteome.
FT INIT_MET 0
FT BINDING 36 36 BIOTIN (BY SIMILARITY).
SQ SEQUENCE 70 AA; 7175 MW; 08B82DDD3A76892D CRC64;

Query Match 33.6%; Score 115; DB 1; Length 70;
Best Local Similarity 37.7%; Pred. No. 0.0001;
Matches 23; Conservative 13; Mismatches 25; Indels 0; Gaps 0;

QY 3 EIPAPLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTGGKVEKVLVKERDAVQG 62
Db 3 DVRAEIVASVLEVVWNEGDQIDKGDVVVLLLESMKMEIPVLAAGTAVSVGVDVQA 62

QY 63 G 63
Db 63 G 63


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RESULT 27
ODP2_MYCCA          STANDARD;          PRT;    438 AA.
AC   Q49110;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   Dihydrolipoamide acetyltransferase component of pyruvate dehydrogenase
DE   complex (EC 2.3.1.12) (E2).
GN   PDHC OR ODP2.
OS   Mycoplasma capricolum.
OC   Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
OX   NCBI_TaxID=2095;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=97001869; PubMed=8844861;
RA   Zhu P.P., Peterkofsky A.;
RT   "Sequence and organization of genes encoding enzymes involved in
RT   pyruvate metabolism in Mycoplasma capricolum.";
RL   Protein Sci. 5:1719-1736(1996).
CC   -!- FUNCTION: THE PYRUVATE DEHYDROGENASE COMPLEX CATALYZES THE OVERALL
CC   CONVERSION OF PYRUVATE TO ACETYL-COA & CO(2). IT CONTAINS MULTIPLE
CC   COPIES OF THREE ENZYMATIC COMPONENTS: PYRUVATE DEHYDROGENASE (E1),
CC   DIHYDROLIPOAMIDE ACETYLTRANSFERASE (E2) & LIPOAMIDE DEHYDROGENASE
CC   (E3) (BY SIMILARITY).
CC   -!- CATALYTIC ACTIVITY: Acetyl-CoA + dihydrolipoamide = CoA + S-
CC   acetyldihydrolipoamide.
CC   -!- COFACTOR: Contains 1 covalently bound lipoyl cofactor (By
CC   similarity).
CC   -!- SUBUNIT: Forms a 24-polypeptide structural core with octahedral
CC   symmetry (By similarity).
CC   -!- SIMILARITY: Belongs to the 2-oxoacid dehydrogenase family.
CC   -!- SIMILARITY: Contains 1 lipoyl-binding domain.
-----
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EMBL; U62057; AAC44344.1; --
DR   HSSP; P07016; 1C4T.
DR   InterPro; IPR001078; 2Oxoacid_dh.
DR   InterPro; IPR000089; Biotin_lipoyl.
DR   InterPro; IPR004167; E3_binding.
DR   InterPro; IPR003016; Lipoyl_BS.
DR   Pfam; PF00198; 2-oxoacid_dh; 1.
DR   Pfam; PF00364; biotin_lipoyl; 1.
DR   Pfam; PF02817; e3 binding; 1.
DR   ProDom; PD001115; 2Oxoacid_dh; 1.
DR   PROSITE; PS00189; LIPOYL; 1.
KW   Glycolysis; Transferase; Acyltransferase; Lipoyl.
FT   BINDING   42 42 LIPOYL (BY SIMILARITY).
FT   ACT_SITE  411 411 POTENTIAL.
SQ   SEQUENCE  438 AA; 46927 MW; 4BF83B697480B4AB CRC64;

Query Match      33.3%; Score 114; DB 1; Length 438;
Best Local Similarity 38.3%; Pred. No. 0.00069;
Matches 23; Conservative 16; Mismatches 21; Indels 0; Gaps 0;

QY   10 GTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVKVVLVKERDAVQGGGLIKI 69
    |||::||| ||| |||:: ||| ||| ||| |||:: |||:: |||:: |||:: |||
Db    16 GTVAEVLVKGDVVKEGQSLYFVETDKVNSEIPAPVAGKIAVINIKAGQEIKVGDDVMEI 75

RESULT 28
ODP2_ECOLI
ID   ODP2_ECOLI          STANDARD;          PRT;    629 AA.
AC   P06959;
DT   01-APR-1988 (Rel. 07, Created)
DT   01-FEB-1995 (Rel. 31, Last sequence update)
```

```
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Dihydrolipoamide acetyltransferase component of pyruvate dehydrogenase
DE   complex (EC 2.3.1.12) (E2).
GN   ACEF OR B0115.
OS   Escherichia coli.
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC   Enterobacteriaceae; Escherichia.
OX   NCBI_TaxID=562;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   STRAIN=K12;
RX   MEDLINE=83234434; PubMed=6345153;
RA   Stephens P.E., Darlison M.G., Lewis H.M., Guest J.R.;
RT   "The pyruvate dehydrogenase complex of Escherichia coli K12.
RT   Nucleotide sequence encoding the dihydrolipoamide acetyltransferase
RT   component.";
RL   Eur. J. Biochem. 133:481-489(1983).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   STRAIN=K12 / MG1655;
RX   MEDLINE=97426617; PubMed=9278503;
RA   Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA   Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA   Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA   Mau B., Shao Y.;
RT   "The complete genome sequence of Escherichia coli K-12.";
RT   Science 277:1453-1474(1997).
RN   [3]
RP   SEQUENCE OF 1-12.
RX   STRAIN=K12 / EMG2;
RX   MEDLINE=97443975; PubMed=9298646;
RA   Link A.J., Robison K., Church G.M.;
RT   "Comparing the predicted and observed properties of proteins encoded
RT   in the genome of Escherichia coli K-12.";
RL   Electrophoresis 18:1259-1313(1997).
RN   [4]
RP   SEQUENCE OF 34-46.
RX   MEDLINE=84256520; PubMed=6821375;
RA   Hale G., Perham R.N.;
RT   "Amino acid sequence around lipoic acid residues in the pyruvate
RT   dehydrogenase multienzyme complex of Escherichia coli.";
RL   Biochem. J. 187:905-908(1980).
RN   [5]
RP   MUTAGENESIS OF HIS-602.
RX   MEDLINE=90351365; PubMed=2201286;
RA   Russel G.C., Guest J.R.;
RT   "Overexpression of restructured pyruvate dehydrogenase complexes and
RT   site-directed mutagenesis of a potential active-site histidine
RT   residue.";
RL   Biochem. J. 269:443-450(1990).
RN   [6]
RP   LIPOYLATED DOMAINS STUDIES.
RX   MEDLINE=91024917; PubMed=2121129;
RA   Ali S.T., Guest J.R.;
RT   "Isolation and characterization of lipoylated and unlipoylated
RT   domains of the E2p subunit of the pyruvate dehydrogenase complex of
RT   Escherichia coli.";
RL   Biochem. J. 271:139-145(1990).
CC   -!- FUNCTION: The pyruvate dehydrogenase complex catalyzes the overall
CC   conversion of pyruvate to acetyl-CoA and CO(2). It contains
CC   multiple copies of three enzymatic components: pyruvate
CC   dehydrogenase (E1), dihydrolipoamide acetyltransferase (E2) and
CC   lipoaamide dehydrogenase (E3).
CC   -!- CATALYTIC ACTIVITY: Acetyl-CoA + dihydrolipoamide = CoA + S-
CC   acetyldihydrolipoamide.
CC   -!- COFACTOR: Contains 3 covalently bound lipoyl cofactors.
CC   -!- SUBUNIT: Forms a 24-polypeptide structural core with octahedral
CC   symmetry.
CC   -!- SIMILARITY: Belongs to the 2-oxoacid dehydrogenase family.
CC   -!- SIMILARITY: Contains 3 lipoyl-binding domains.
-----
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DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Propionyl-CoA carboxylase alpha chain, mitochondrial precursor
DE (EC 6.4.1.3) (PCCase alpha subunit) (Propanoyl-CoA:carbon dioxide
DE ligase alpha subunit).
GN PCCA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89296507; PubMed=2740237;
RA Lamhonwah A.-M., Mahuran D.J., Gravel R.A.;
RT "Human mitochondrial propionyl-CoA carboxylase: localization of the
RT N-terminus of the pro- and mature alpha chains in the deduced
RT primary sequence of a full-length cDNA.";
RL Nucleic Acids Res. 17:4396-4396(1989).
RN [2]
RP REVISIONS.
RA Gravel R.A.;
RL Submitted (APR-1993) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Campeau E., Desviat L.R., Leclerc D., Perez B., Ugarte M.,
RA Gravel R.A.;
RT "Structure of the PCCA gene and distribution of mutations in propionic
RT acidemia";
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [5]
RP SEQUENCE OF 344-536 FROM N.A.
RX MEDLINE=86259695; PubMed=3460076;
RA Lamhonwah A.-M., Barankiewicz T.J., Willard H.F., Mahuran D.J.,
RA Quan F., Gravel R.A.;
RT "Isolation of cDNA clones coding for the alpha and beta chains of
RT human propionyl-CoA carboxylase: chromosomal assignments and DNA
RT polymorphisms associated with PCCA and PCCB genes.";
RL Proc. Natl. Acad. Sci. U.S.A. 83:4864-4868(1986).
RN [6]
RP SEQUENCE OF 339-367 FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=93167265; PubMed=8434582;
RA Stankovics J., Ledley F.D.;
RT "Cloning of functional alpha propionyl CoA carboxylase and correction
RT of enzyme deficiency in pcca fibroblasts.";
RL Am. J. Hum. Genet. 52:144-151(1993).
RN [7]
RP SEQUENCE OF 608-703 FROM N.A.
RX MEDLINE=87212051; PubMed=3555348;
RA Lamhonwah A.-M., Quan F., Gravel R.A.;

RT "Sequence homology around the biotin-binding site of human
RT propionyl-CoA carboxylase and pyruvate carboxylase.";
RL Arch. Biochem. Biophys. 254:631-636(1987).
RN [8]
RP REVIEW ON PA VARIANTS.
RX MEDLINE=99433966; PubMed=10502773;
RA Ugarte M., Perez-Cerda C., Rodriguez-Pombo P., Desviat L.R., Perez B.,
RA Richard E., Muro S., Campeau E., Ohura T., Gravel R.A.;
RT "Overview of mutations in the PCCA and PCCB genes causing propionic
RT acidemia";
RL Hum. Mutat. 14:275-282(1999).
RN [9]
RP VARIANTS PA-1 TRP-52; THR-113; THR-139; LYS-348 AND ARG-606.
RX MEDLINE=99203168; PubMed=10101253;
RA Richard E., Desviat L.R., Perez B., Perez-Cerda C., Ugarte M.;
RT "Genetic heterogeneity in propionic acidemia patients with alpha-
RT subunit defects: identification of five novel mutations, one of them
RT causing instability of the protein.";
RL Biochim. Biophys. Acta 1453:351-358(1999).
RN [10]
RP VARIANTS PA-1 PRO-50; LYS-204; GLY-343; VAL-354; ARG-643 AND CYS-687
DEL.
RX MEDLINE=99263311; PubMed=10329019;
RA Campeau E., Dupuis L., Leon-Del-Rio A., Gravel R.;
RT "Coding sequence mutations in the alpha subunit of propionyl-CoA
RT carboxylase in patients with propionic acidemia.";
RL Mol. Genet. Metab. 67:11-22(1999).
CC -I- CATALYTIC ACTIVITY: ATP + propanoyl-CoA + HCO(3) (-) = ADP +
CC phosphate + (S)-methylmalonyl-CoA.
CC -I- COFACTOR: Biotin.
CC -I- PATHWAY: Key enzyme in the catabolic pathway of odd-chain fatty
CC acids, isoleucine, threonine, methionine, and valine.
CC -I- SUBUNIT: Probably a dodecamer composed of six biotin-containing
CC alpha subunits and six beta subunits.
CC -I- SUBCELLULAR LOCATION: Mitochondrial matrix.
CC -I- DISEASE: Defects in PCCA are the cause of propionic acidemia type
CC I (PA-1) [MIM:606054]. PA-1 is a life-threatening disease
CC characterized by episodic vomiting, lethargy and ketosis,
CC neutropenia, periodic thrombocytopenia, hypogammaglobulinemia,
CC developmental retardation, and intolerance to protein.
CC -----
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CC -----
DR EMBL; X14608; CAA32763.1; -
DR EMBL; AY035808; AAK61392.1; -
DR EMBL; AY035786; AAK61392.1; JOINED.
DR EMBL; AY035787; AAK61392.1; JOINED.
DR EMBL; AY035788; AAK61392.1; JOINED.
DR EMBL; AY035789; AAK61392.1; JOINED.
DR EMBL; AY035790; AAK61392.1; JOINED.
DR EMBL; AY035791; AAK61392.1; JOINED.
DR EMBL; AY035792; AAK61392.1; JOINED.
DR EMBL; AY035793; AAK61392.1; JOINED.
DR EMBL; AY035794; AAK61392.1; JOINED.
DR EMBL; AY035795; AAK61392.1; JOINED.
DR EMBL; AY035796; AAK61392.1; JOINED.
DR EMBL; AY035797; AAK61392.1; JOINED.
DR EMBL; AY035798; AAK61392.1; JOINED.
DR EMBL; AY035799; AAK61392.1; JOINED.
DR EMBL; AY035800; AAK61392.1; JOINED.
DR EMBL; AY035801; AAK61392.1; JOINED.
DR EMBL; AY035802; AAK61392.1; JOINED.
DR EMBL; AY035803; AAK61392.1; JOINED.
DR EMBL; AY035804; AAK61392.1; JOINED.
DR EMBL; AY035805; AAK61392.1; JOINED.
DR EMBL; AY035806; AAK61392.1; JOINED.
DR EMBL; AY035807; AAK61392.1; JOINED.

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DR EMBL; BC000140; AAH00140.1; -.
DR EMBL; M13572; AAA60035.1; -.
DR EMBL; S55656; AAB25345.1; -.
DR EMBL; M26121; AAA36424.1; -.
DR PIR; S04613; A27883.
DR HSSP; P24182; IDV1.
DR Genew; HGNC:8653; PCCA.
DR GK; P05165; -.
DR MIM; 232000; -.
DR MIM; 606054; -.
DR GO; GO:0009374; F:biotin binding; TAS.
DR GO; GO:0004658; F:propionyl-CoA carboxylase activity; TAS.
DR InterPro; IPR001882; Biotin_BS.
DR InterPro; IPR005482; Biotin_carb_C.
DR InterPro; IPR000089; Biotin_lipoyl.
DR InterPro; IPR005479; CPase_L_D2.
DR InterPro; IPR005481; CPase_L_N.
DR Pfam; PF02785; Biotin_carb_C; 1.
DR Pfam; PF00364; biotin_lipoyl; 1.
DR Pfam; PF00289; CPSase_L_chain; 1.
DR Pfam; PF02786; CPSase_L_D2; 1.
DR PROSITE; PS00188; BIOTIN; 1.
DR PROSITE; PS00867; CPSASE_1; 1.
DR PROSITE; PS00867; CPSASE_2; 1.
DR Mitochondrion; Ligase; Biotin; ATP-binding; Transit peptide;
KW Disease mutation; Polymorphism.
FT TRANSIT 1 20 MITOCHONDRION.
FT CHAIN 21 703 PROPIONYL-COA CARBOXYLASE ALPHA CHAIN.
FT NP BIND 198 203 ATP (POTENTIAL).
FT ACT SITE 328 328 BY SIMILARITY.
FT BINDING 669 669 BIOTIN (BY SIMILARITY).
FT VARIANT 50 50 A -> P (in PA-1).
FT VARIANT 52 52 R -> W (in PA-1).
FT VARIANT 113 113 A -> T (in PA-1).
FT VARIANT 139 139 I -> T (in PA-1).
FT VARIANT 204 204 M -> K (in PA-1).
FT VARIANT 272 272 Q -> R (in PA-1).
FT VARIANT 343 343 D -> G (in PA-1).
FT VARIANT 348 348 M -> K (in PA-1; unstable protein).
FT VARIANT 354 354 G -> V (in PA-1).
FT VARIANT 374 374 R -> Q (in PA-1).
Query Match 32.2%; Score 110; DB 1; Length 703;
Best Local Similarity 37.5%; Pred. No. 0.0026;
Matches 24; Conservative 12; Mismatches 28; Indels 0; Gaps 0;
QY 6 APLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTGDGKVEKVLVKERDAVQGGQG 65
Db 639 SPMPGVVAVSVKPGDAVAEGQIEICVIEAMKQNSMTAGKTGTGTVKSVHCQAGDVTGEGDL 698
QY 66 LIKI 69
Db 699 LVEL 702
RESULT 31
BCCP_CHLPN STANDARD; PRT; 167 AA.
AC Q9Z901;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Biotin carboxyl carrier protein of acetyl-CoA carboxylase (BCCP).
GN ACCB OR CPN0183 OR CP0585 OR CPB0186.
```

```
OS Chlamydia pneumoniae (Chlamydophila pneumoniae).
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydophila.
OX NCBI_TaxID=83558;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CWL029;
RX MEDLINE=99206606; PubMed=10192388;
RA Kalman S., Mitchell W., Marathe R., Lammel C., Fan J., Hyman R.W.,
RA Olinger L., Grimwood J., Davis R.W., Stephens R.S.;
RT "Comparative genomes of Chlamydia pneumoniae and C. trachomatis.";
RL Nat. Genet. 21:385-389(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=AR39;
RX MEDLINE=20150255; PubMed=10684935;
RA Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
RA White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S.,
RA Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,
RA Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.,
RA Eisen J., Fraser C.M.;
RT "Genome sequences of Chlamydia trachomatis MoPn and Chlamydia
RT pneumoniae AR39.";
RL Nucleic Acids Res. 28:1397-1406(2000).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=J138;
RX MEDLINE=20330349; PubMed=10871362;
RA Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K.,
RA Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.;
RT "Comparison of whole genome sequences of Chlamydia pneumoniae J138
RT from Japan and CWL029 from USA.";
RL Nucleic Acids Res. 28:2311-2314(2000).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=TW-183;
RA Geng M.M., Schumacher A., Muehldorfer I., Bensch K.W., Schaefer K.P.,
RA Schneider S., Pohl T., Essig A., Marre R., Melchers K.;
RT "The genome sequence of Chlamydia pneumoniae TW183 and comparison with
RT other Chlamydia strains based on whole genome sequence analysis.";
RL Submitted (MAY-2002) to the EMBL/GenBank/DBSJ databases.
CC -!- FUNCTION: This protein is a component of the acetyl coenzyme A
CC carboxylase complex; first, biotin carboxylase catalyzes the
CC carboxylation of the carrier protein and then the transcarboxylase
CC transfers the carboxyl group to form malonyl-CoA (By similarity).
CC -!- PATHWAY: Long-chain fatty acid biosynthesis; first step.
CC -!- SUBUNIT: Homodimer (By similarity).
CC -----
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CC -----
DR EMBL; AE001604; AAD18336.1; -.
DR EMBL; AE002217; AAF38403.1; -.
DR EMBL; AF002545; BAA98393.1; -.
DR EMBL; AE017157; AAP98119.1; -.
DR PIR; F72110; F72110.
DR PIR; G86513; G86513.
DR HSSP; P02905; 3EDO.
DR PHCI-2DPAGE; Q9Z901; -.
DR TIGR; CP0585; -.
DR InterPro; IPR001249; AcCoA_biotinCC.
DR InterPro; IPR001882; Biotin_BS.
DR InterPro; IPR000089; Biotin_lipoyl.
DR Pfam; PF00364; biotin_lipoyl; 1.
DR PRINTS; PR01071; ACOAB10TINCC.
DR TIGRFAMs; TIGR00531; BCCP; 1.
DR PROSITE; PS00188; BIOTIN; 1.
KW Fatty acid biosynthesis; Biotin; Complete proteome.
FT BINDING 129 129 BIOTIN (BY SIMILARITY).
```



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DR EMBL; Y12884; CAA73385.1; -.
DR EMBL; AF086791; AAC70362.1; -.
DR HSSP; P09061; IQS0.
DR InterPro; IPR000089; Biotin_lipoyl.
DR InterPro; IPR003016; Lipoyl_BS.
DR InterPro; IPR009014; Transketolase_C.
DR InterPro; IPR005476; Transketolase_C.
DR InterPro; IPR005475; Transketolase_CR.
DR Pfam; PF00364; biotin_lipoyl; 1.
DR Pfam; PF02779; transket_pyr; 1.
DR Pfam; PF02780; transketolase_C; 1.
DR PROSITE; PS00189; LIPOYL; 1.
KW Glycolysis; Oxidoreductase; Flavoprotein; Thiamine pyrophosphate;
KW Lipoyl.
FT BINDING 43 43 LIPOYL (POTENTIAL).
FT CONFLICT 87 87 E -> D (IN REF. 2).
FT CONFLICT 112 112 L -> V (IN REF. 2).
FT CONFLICT 232 244 SAAKTHYMSGGV -> LRPKRIICPAKC (IN REF. 2).
FT CONFLICT 259 259 R -> P (IN REF. 2).
FT CONFLICT 262 262 A -> E (IN REF. 2).
FT SEQUENCE 462 AA; 49860 MW; 514275F7D70C34BC CRC64;
SQ
Query Match 30.1%; Score 103; DB 1; Length 462;
Best Local Similarity 34.8%; Pred. No. 0.0083;
Matches 23; Conservative 14; Mismatches 23; Indels 6; Gaps 1;
QY 5 PAPLAGTVSKLVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVLKRDVQGGQ 64
Db 12 PTMEEGTLRWLVKEGDSIKAGEILAEIETDKAIMEFEAVDEGVITKILPE-----GS 65
QY 65 GLIKIG 70
Db 66 ENVKVG 71
RESULT 37
BCCP_HAEIN
ID BCCP_HAEIN STANDARD; PRT; 155 AA.
AC P43874;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Biotin carboxyl carrier protein of acetyl-CoA carboxylase (BCCP).
GN ACCB OR FABB OR HI0971.
OS Haemophilus influenzae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Haemophilus.
OX NCBI_TaxID=727;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Rd / KW20 / ATCC 51907;
RX MEDLINE=95350630; PubMed=7542800;
RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
RA Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
RA McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
RA Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
RA Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
RA Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
RA Venter J.C.;
RT "Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.";
RL Science 269:496-512(1995).
RN [2]
RP SEQUENCE OF 1-10.
RX MEDLINE=20137488; PubMed=10675023;
RA Langen H., Takacs B., Evers S., Berndt P., Lahm H.W., Wipf B.,
RA Gray C., Fountoulakis M.;
RT "Two-dimensional map of the proteome of Haemophilus influenzae.";
RL Electrophoresis 21:411-429(2000).
CC -!- FUNCTION: This protein is a component of the acetyl coenzyme A
```

```
CC carboxylase complex; first, biotin carboxylase catalyzes the
CC carboxylation of the carrier protein and then the transcarboxylase
CC transfers the carboxyl group to form malonyl-CoA (By similarity).
CC -!- PATHWAY: Long-chain fatty acid biosynthesis; first step.
CC -!- SUBUNIT: Homodimer (By similarity).
CC
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CC
CC EMBL; U32778; AAC22631.1; -.
CC PIR; E64105; E64105.
CC HSSP; P02905; 1BDO.
CC TIGR; HI0971; -.
CC InterPro; IPR001249; AcCoA_biotinCC.
CC InterPro; IPR001882; Biotin_BS.
CC InterPro; IPR000089; Biotin_lipoyl.
CC Pfam; PF00364; biotin_lipoyl; 1.
CC PRINTS; PR01071; ACOABIOTINCC.
CC TIGRFAMS; TIGR00531; BCCP; 1.
CC PROSITE; PS00188; BIOTIN; 1.
KW Fatty acid biosynthesis; Biotin; Complete proteome.
FT BINDING 121 121 BIOTIN (BY SIMILARITY)..
SQ SEQUENCE 155 AA; 16247 MW; 696F19B4429A03CD CRC64;
Query Match 30.0%; Score 102.5; DB 1; Length 155;
Best Local Similarity 32.9%; Pred. No. 0.0034;
Matches 24; Conservative 16; Mismatches 26; Indels 7; Gaps 1;
QY 4 IPAPLAGTV-----SKLVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVLVKE 56
Db 82 VRSPMVGTFRSPSPSEAKAFVEVGQSVKVGDAICIVEAMKMMNRIEADKAGVVKAILND 141
QY 57 RDAVQGGQGLIKI 69
Db 142 GNAVEFDEPLVI 154
RESULT 38
ODP2_ACHLA
ID ODP2_ACHLA STANDARD; PRT; 544 AA.
AC P35489;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Dihydrolipoamide acetyltransferase component of pyruvate dehydrogenase
DE complex (EC 2.3.1.12) (E2).
GN PDHC.
OS Acholeplasma laidlawii.
OC Bacteria; Firmicutes; Mollicutes; Acholeplasmatales;
OC Acholeplasmataceae; Acholeplasma.
OX NCBI_TaxID=2148;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX MEDLINE=92138635; PubMed=1735725;
RA Wallbrant P., Tegman V., Jonsson B.-H., Wieslander A.;
RT "Identification and analysis of the genes coding for the putative
RT pyruvate dehydrogenase enzyme complex in Acholeplasma laidlawii.";
RL J. Bacteriol. 174:1388-1396(1992).
CC -!- FUNCTION: The pyruvate dehydrogenase complex catalyzes the overall
CC conversion of pyruvate to acetyl-CoA and CO(2). It contains
CC multiple copies of three enzymatic components: pyruvate
CC dehydrogenase (E1), dihydrolipoamide acetyltransferase (E2) and
CC lipoamide dehydrogenase (E3).
CC -!- CATALYTIC ACTIVITY: Acetyl-CoA + dihydrolipoamide = CoA + S-
CC acetyldihydrolipoamide.
CC -!- COFACTOR: Contains 2 covalently bound lipoyl cofactors
CC (Potential).
CC -!- SUBUNIT: Forms a 24-polypeptide structural core with octahedral
```

```
CC symmetry (By similarity).
CC -!- SIMILARITY: Belongs to the 2-oxoacid dehydrogenase family.
CC -!- SIMILARITY: Contains 2 lipoyl-binding domains.
CC -----
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CC -----
CC EMBL; M81753; AAA21909.1; -.
CC PIR; C42653; C42653.
CC HSSP; P07016; 1C4T.
CC InterPro; IPR001078; 2Oxoacid dh.
CC InterPro; IPR000089; Biotin lipoyl.
CC InterPro; IPR004167; E3 binding.
CC InterPro; IPR003016; Lipoyl BS.
CC Pfam; PF00198; 2-oxoacid dh; 1.
CC Pfam; PF00364; biotin lipoyl; 2.
CC Pfam; PF02817; e3 binding; 1.
CC ProDom; PD001115; 2Oxoacid dh; 1.
CC PROSITE; PS00189; LIPOYL; 2.
CC Glycolysis; Transferase; Acyltransferase; Lipoyl.
KW BINDING 42 42 LIPOYL (BY SIMILARITY).
FT BINDING 154 154 LIPOYL (BY SIMILARITY).
FT ACT SITE 516 516 POTENTIAL.
SQ SEQUENCE 544 AA; 57261 MW; 81E92D869CFD5424 CRC64;

Query Match 29.8%; Score 102; DB 1; Length 544;
Best Local Similarity 35.0%; Pred. No. 0.012;
Matches 21; Conservative 15; Mismatches 24; Indels 0; Gaps 0;

QY 10 GTVSKILVKEGDTVKAGTQVLVLEAMKMETEINAPTDGKVEKVLVKERDAVGGQGLIKI 69
Db 16 GTVLQWNFKVGDVKVEGETLVIVETDKVNAELSPVDGTIVSLGAKEGEIHVGQIIVTI 75

RESULT 39
ODP2_AZOVI STANDARD; PRT; 637 AA.
AC P10802;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Dihydrolipoamide acetyltransferase component of pyruvate dehydrogenase
DE complex (EC 2.3.1.12) (E2).
OS Azotobacter vinelandii.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Azotobacter.
OX NCBI_TaxID=354;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 478;
RX MEDLINE=88271330; PubMed=3292237;
RA Hanemaaijer R., Janssen A., de Kok A., Jolles J., Veeger C.;
RT "The dihydrolipoyltransferase component of the pyruvate
RT dehydrogenase complex from Azotobacter vinelandii. Molecular cloning
RT and sequence analysis.";
RL Eur. J. Biochem. 174:593-599(1988).
RN [2]
RP SEQUENCE OF 1-15 AND 380-415.
RX MEDLINE=88082750; PubMed=3691494;
RA Hanemaaijer R., de Kok A., Jolles J., Veeger C.;
RT "The domain structure of the dihydrolipoyl transferase component
RT of the pyruvate dehydrogenase complex from Azotobacter vinelandii.";
RL Eur. J. Biochem. 169:245-252(1987).
RN [3]
RP LIPOYL DOMAIN CONFORMATION.
RX MEDLINE=89052887; PubMed=3191993;
RA Hanemaaijer R., Vervoort J., Westphal A.H., de Kok A., Veeger C.;
RT "Mobile sequences in the pyruvate dehydrogenase complex, the E2
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RT component, the catalytic domain and the 2-oxoglutarate dehydrogenase
RT complex of Azotobacter vinelandii, as detected by 600 MHz 1H-NMR
RT spectroscopy.";
RL FEBS Lett. 240:205-210(1988).
RN [4]
RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF 381-637.
RX MEDLINE=92196586; PubMed=1549782;
RA Mattevi A., Obmolova G., Schulze E., Kalk K.H., Westphal A.H.,
RA de Kok A., Hol W.G.J.;
RT "Atomic structure of the cubic core of the pyruvate dehydrogenase
RT multienzyme complex.";
RL Science 255:1544-1550(1992).
RN [5]
RP STRUCTURE BY NMR OF 1-78.
RX MEDLINE=94222112; PubMed=8068086;
RA Berg A., de Kok A., Vervoort J.;
RT "Sequential 1H and 15N nuclear magnetic resonance assignments and
RT secondary structure of the N-terminal lipoyl domain of the
RT dihydrolipoyl transferase component of the pyruvate dehydrogenase
RT complex from Azotobacter vinelandii.";
RL Eur. J. Biochem. 221:87-100(1994).
RN [6]
RP STRUCTURE BY NMR OF 1-78.
RX MEDLINE=97234563; PubMed=9119000;
RA Berg A., Vervoort J., de Kok A.;
RT "Three-dimensional structure in solution of the N-terminal lipoyl
RT domain of the pyruvate dehydrogenase complex from Azotobacter
RT vinelandii.";
RL Eur. J. Biochem. 244:352-360(1997).
CC -!- FUNCTION: The pyruvate dehydrogenase complex catalyzes the overall
CC conversion of pyruvate to acetyl-CoA and CO(2). It contains
CC multiple copies of three enzymatic components: pyruvate
CC dehydrogenase (E1), dihydrolipoamide acetyltransferase (E2) and
CC lipoamide dehydrogenase (E3).
CC -!- CATALYTIC ACTIVITY: Acetyl-CoA + dihydrolipoamide = CoA + S-
CC acetyldihydrolipoamide.
CC -!- COFACTOR: Contains 3 covalently bound lipoyl cofactors (By
CC similarity).
CC -!- SUBUNIT: Forms a 24-polypeptide structural core with octahedral
CC symmetry.
CC -!- SIMILARITY: Belongs to the 2-oxoacid dehydrogenase family.
CC -!- SIMILARITY: Contains 3 lipoyl-binding domains.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC -----
CC EMBL; X12455; CAA30987.1; ALT_INIT.
CC PIR; S01017; XXAV.
CC PDB; 1EAA; 31-OCT-93.
CC PDB; 1EAB; 31-OCT-93.
CC PDB; 1EAC; 31-OCT-93.
CC PDB; 1EAD; 31-OCT-93.
CC PDB; 1EAE; 31-OCT-93.
CC PDB; 1EAF; 31-OCT-93.
CC PDB; 1IYU; 12-MAR-97.
CC PDB; 1IYV; 12-MAR-97.
CC PDB; 1DPB; 20-APR-95.
CC PDB; 1DPC; 20-APR-95.
CC PDB; 1DPD; 20-APR-95.
CC InterPro; IPR001078; 2Oxoacid dh.
CC InterPro; IPR006256; AceF.
CC InterPro; IPR000089; Biotin lipoyl.
CC InterPro; IPR004167; E3 binding.
CC InterPro; IPR003016; Lipoyl_BS.
CC Pfam; PF00198; 2-oxoacid dh; 1.
CC Pfam; PF00364; biotin lipoyl; 3.
CC Pfam; PF02817; e3 binding; 1.
CC ProDom; PD001115; 2Oxoacid dh; 1.
```


GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 3, 2004, 10:25:29 ; Search time 25.8854 Seconds
(without alignments).
853.232 Million cell updates/sec

Title: US-09-987-485A-2
Perfect score: 342
Sequence: 1 EGEIPAPLAGTVSKILVKEG.....KVLVKERDAVQGGQLIKIG 70

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTRMBL_25.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phage.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_rvirus.*
- 16: sp_bacteriap.*
- 17: sp_archaea.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	214	62.6	120	16	Q8FRF4 corynebacte
2	195	57.0	145	17	Q9V0A6 pyrococcus
3	189	55.3	149	17	Q59021 pyrococcus
4	181	52.9	144	17	Q8U303 pyrococcus
5	180	52.6	571	17	O58564 pyrococcus
6	178	52.0	140	17	O28067 pyrococcus
7	178	52.0	986	16	Q891Y8 archaeoglob
8	174	50.9	655	16	O67484 aquifex aeo
9	174	50.9	984	2	Q9XBJ1 bacillus ce
10	174	50.9	1148	16	Q81MT6 bacillus an
11	174	50.9	1148	16	Q819M9 bacillus ce
12	170	49.7	186	17	Q97VY7 sulfolobus
13	167	48.8	134	16	Q9WZH6 thermotoga
14	167	48.8	596	2	Q48826 legionella
15	167	48.8	1144	16	Q97FR7 clostridium
16	165	48.2	167	1	Q8J2Z3 metallospha

17	165	48.2	1144	16	Q88VC5	Q88vc5 lactobacill
18	164	48.0	597	16	Q9KUH1	Q9kuh1 vibrio chol
19	163	47.7	599	16	Q9PP00	Q9pp00 campylobact
20	161	47.1	142	17	O28194	O28194 archaeoglob
21	160	46.8	602	16	Q87U07	Q87u07 pseudomonas
22	159.5	46.6	576	16	Q8U917	Q8u917 agrobacteri
23	159	46.5	144	16	Q8A737	Q8a737 bacteroides
24	159	46.5	602	16	Q88C37	Q88c37 pseudomonas
25	159	46.5	665	16	Q92H13	Q92h13 rickettsia
26	158	46.2	169	17	Q974R8	Q974r8 sulfolobus
27	158	46.2	607	16	Q9HTD1	Q9htd1 pseudomonas
28	157	45.9	1146	16	Q92CW1	Q92cw1 listeria in
29	157	45.9	1146	16	Q8Y846	Q8y846 listeria mo
30	157	45.9	1150	16	Q9K9M0	Q9k9m0 bacillus ha
31	156.5	45.8	1140	2	Q8L2G4	Q8l2g4 corynebacte
32	156	45.6	116	16	Q99ZL6	Q99zl6 streptococc
33	156	45.6	116	16	Q8K7G1	Q8k7g1 streptococc
34	155.5	45.5	1139	2	Q8RQL2	Q8rql2 corynebacte
35	155.5	45.5	1140	16	O54587	O54587 corynebacte
36	155.5	45.5	1168	16	Q8FRQ0	Q8frq0 corynebacte
37	155	45.3	116	16	Q8P104	Q8p104 streptococc
38	153	44.7	135	16	Q8RAJ2	Q8raj2 thermoanaer
39	153	44.7	620	16	O67544	O67544 aquifex aeo
40	152	44.4	167	1	O52603	O52603 sulfolobus
41	152	44.4	167	1	Q877I4	Q877i4 acidianus b
42	152	44.4	436	10	Q40121	Q40121 lycopersico
43	152	44.4	595	16	Q87LR7	Q87lr7 vibrio para
44	151	44.2	157	16	Q8K630	Q8k630 streptococc
45	151	44.2	166	16	Q99YD8	Q99yd8 streptococc

ALIGNMENTS

RESULT 1

Q8FRF4 ID Q8FRF4 PRELIMINARY; PRT; 120 AA.
AC Q8FRF4;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Putative biotin carboxyl carrier protein.
GN CE0807.
OS Corynebacterium efficiens.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Corynebacteriaceae; Corynebacterium.
OX NCBI_TaxID=152794;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=YS-314 / AJ 12310 / DSM 44549 / JCM 11189;
RA Kawarabayasi Y., Yamazaki J., Hino Y., Kikuchi H., Nakamura Y.,
RA Ikeo K., Suzuki M., Mashima J., Itoh T., Yamagishi A., Nishio Y.,
RA Usuda Y., Sugimoto S.;
RT "The entire genomic sequence of Corynebacterium efficiens YS-314.";
RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AP005216; BAC17617.1; -;
DR GO; GO:0009374; F:biotin binding; IEA.
DR InterPro; IPR001882; Biotin_BS.
DR InterPro; IPR000089; Biotin_lipoyl.
DR Pfam; PF00364; biotin_lipoyl; 1.
DR PROSITE; PS00188; BIOTIN; 1.
KW Complete proteome.
SQ SEQUENCE 120 AA; 12298 MW; 4C36E4AB41C969E5 CRC64;

Query Match 62.6%; Score 214; DB 16; Length 120;
Best Local Similarity 68.2%; Pred. No. 1.1e-14;
Matches 45; Conservative 9; Mismatches 12; Indels 0; Gaps 0;
QY 4 IPAPLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVLVKERDAVQGG 63
DB 54 VVAPLAGSVFKILVAEGDTIEAGQVLLVLEAMKMETEITAPSGVVGVGAINVKEGAVQGG 113
QY 64 QGLIKI 69

Db 114 QSLIEI 119

RESULT 2

Q9V0A6 PRELIMINARY; PRT; 145 AA.

AC Q9V0A6;

DT 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Methylmalonyl-CoA decarboxylase gamma chain.

GN PYRAB08850 OR PAB1771.

OS Pyrococcus abyssi.

OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;

OC Pyrococcus.

OX NCBI_TaxID=29292;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=GE5 / Orsay;

RA Heilig R.;

RT "Pyrococcus abyssi genome sequence: insights into archaeal chromosome structure and evolution.";

RT Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.

RL EMBL; AJ248285; CAB49799.1; --

DR PIR; F75135; F75135.

DR HSSP; P02905; 1BDO.

DR GO; GO:0009374; F:biotin binding; IEA.

DR InterPro; IPR001882; Biotin_BS.

DR InterPro; IPR000089; Biotin_lipoyl.

DR Pfam; PF00364; biotin_lipoyl; 1.

DR PROSITE; PS00188; BIOTIN; 1.

KW Complete proteome.

SQ SEQUENCE 145 AA; 15489 MW; 9C14433663F40D94 CRC64;

Query Match 57.0%; Score 195; DB 17; Length 145;

Best Local Similarity 58.6%; Pred. No. 1.3e-12;

Matches 41; Conservative 10; Mismatches 19; Indels 0; Gaps 0;

QY 1 EGEIPAPLAGTVSKILVKEGDTVKGQTVLVLEAMKMETEINAPTGDGKVEKVLVKERDAV 60

Db 76 ENVVTAPMPGKVLKILVQEGQVKGQVKGQGLLILEAMKMEINAPRDRGVVVKRILVKEGDAV 135

QY 61 QGGQGLIKIG 70

Db 136 DTGTPLELG 145

RESULT 3

O59021 PRELIMINARY; PRT; 149 AA.

AC O59021;

DT 01-AUG-1998 (TrEMBLrel. 07, Created)

DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE 149AA long hypothetical methylmalonyl-CoA decarboxylase gamma chain.

GN PH1284.

OS Pyrococcus horikoshii.

OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;

OC Pyrococcus.

OX NCBI_TaxID=53953;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=OT3;

RX MEDLINE=98344137; PubMed=9679194;

RA Kawarabayashi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y., Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y., Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y., Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A., Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K., Masuchi Y., Shizuya H., Kakuchi H.;

RT "Complete sequence and gene organization of the genome of a hyperthermophilic archaeobacterium, Pyrococcus horikoshii OT3.";

RL DNA Res. 5:55-76(1998).

DR EMBL; AP000005; BAA30387.1; --

DR PIR; A71074; A71074.

DR HSSP; P10802; 1IYU.

DR GO; GO:0009374; F:biotin binding; IEA.

DR InterPro; IPR001882; Biotin_BS.

DR InterPro; IPR000089; Biotin_lipoyl.

DR Pfam; PF00364; biotin_lipoyl; 1.

DR PROSITE; PS00188; BIOTIN; 1.

KW Complete proteome.

SQ SEQUENCE 149 AA; 15985 MW; 1C3AA5F47E6BA6F1 CRC64;

Query Match 55.3%; Score 189; DB 17; Length 149;

Best Local Similarity 54.3%; Pred. No. 5.7e-12;

Matches 38; Conservative 14; Mismatches 18; Indels 0; Gaps 0;

QY 1 EGEIPAPLAGTVSKILVKEGDTVKGQTVLVLEAMKMETEINAPTGDGKVEKVLVKERDAV 60

Db 80 ENVVSAPMPGKVLRLVVRGDRVRVGGQLLVLEAMKMEINAPRDRGVVVKRILVKEGDAV 139

QY 61 QGGQGLIKIG 70

Db 140 DTGQPLIELG 149

RESULT 4

O8U303 PRELIMINARY; PRT; 144 AA.

AC O8U303;

DT 01-JUN-2002 (TrEMBLrel. 21, Created)

DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Methylmalonyl-CoA decarboxylase gamma chain.

GN PF0673.

OS Pyrococcus furiosus.

OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;

OC Pyrococcus.

OX NCBI_TaxID=2261;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=Vc1 / DSM 3638 / ATCC 43587 / JCM 8422;

RA Weiss R.B., Dunn D.M., Robb F.T., Brown J.R.;

RT "The complete sequence of the Pyrococcus furiosus genome.";

RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AE010188; AAL80797.1; --

DR GO; GO:0009374; F:biotin binding; IEA.

DR InterPro; IPR001882; Biotin_BS.

DR InterPro; IPR000089; Biotin_lipoyl.

DR Pfam; PF00364; biotin_lipoyl; 1.

DR PROSITE; PS00188; BIOTIN; 1.

KW Complete proteome.

SQ SEQUENCE 144 AA; 15315 MW; 422C96A8ED809C6A CRC64;

Query Match 52.9%; Score 181; DB 17; Length 144;

Best Local Similarity 55.2%; Pred. No. 3.7e-11;

Matches 37; Conservative 10; Mismatches 20; Indels 0; Gaps 0;

QY 4 IPAPLAGTVSKILVKEGDTVKGQTVLVLEAMKMETEINAPTGDGKVEKVLVKERDAVQGG 63

Db 78 VTAPMPGKILVSEGQRTVIGQGLLILEAMKMEINAPRDRGVVVKRILVKEGDTVDTG 137

QY 64 QGLIKIG 70

Db 138 QPLIELG 144

RESULT 5

O58564 PRELIMINARY; PRT; 571 AA.

AC O58564;

DT 01-AUG-1998 (TrEMBLrel. 07, Created)

DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE 571AA long hypothetical oxaloacetate decarboxylase alpha chain.
GN PH0834.
OS Pyrococcus horikoshii.
OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
OC Pyrococcus.
OX NCBI_TaxID=53953;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=OT3;
RX MEDLINE=98344137; PubMed=9679194;
RA Kawarabayashi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y.,
RA Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y.,
RA Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y.,
RA Funahashi T., Tanaka T., Kudo Y., Yamazaki J., Kushida N., Oguchi A.,
RA Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,
RA Masuchi Y., Shizuya H., Kikuchi H.;
RT "Complete sequence and gene organization of the genome of a hyper-
thermophilic archaeobacterium, Pyrococcus horikoshii OT3.";
RL DNA Res. 5:55-76(1998).
DR EMBL; AP000003; BAA29928.1; -.
DR FIR; F71133; F71133.
DR HSSP; P02905; 1BDO.
DR GO; GO:0009374; F:biotin binding; IEA.
DR GO; GO:0003824; F:catalytic activity; IEA.
DR GO; GO:0008948; F:oxaloacetate decarboxylase activity; IEA.
DR GO; GO:0006814; P:sodium ion transport; IEA.
DR InterPro; IPR001882; Biotin_BS.
DR InterPro; IPR000089; Biotin_lipoyl.
DR InterPro; IPR000891; HMGL-like.
DR InterPro; IPR005776; Oada.
DR InterPro; IPR003379; PYC OADA.
DR Pfam; PF00364; biotin_lipoyl; 1.
DR Pfam; PF00682; HMGL-like; 1.
DR Pfam; PF02436; PYC OADA; 1.
DR TIGRFAMs; TIGR01108; oada; 1.
DR PROSITE; PS00188; BIOTIN; 1.
KW Complete proteome.
SQ SEQUENCE 571 AA; 64748 MW; B308B0B1C0E5B103 CRC64;
Query Match 52.6%; Score 180; DB 17; Length 571;
Best Local Similarity 54.5%; Pred. No. 2.3e-10;
Matches 36; Conservative 14; Mismatches 16; Indels 0; Gaps 0;
QY 4 IPAPLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTGGKVEKVLVKERDAVQGG 63
Db 505 VSAPMPGKVLRLVVRGDRVRVGGQLLVLEAMKMEINPSPRDGVVVKRLVKEGEAVDTG 564
QY 64 QGLIKI 69
Db 565 QPLIEL 570
RESULT 6
O28067 PRELIMINARY; PRT; 140 AA.
AC O28067;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Methylmalonyl-CoA decarboxylase, biotin carrier subunit
DE (NMDC).
GN AF2216.
OS Archaeoglobus fulgidus.
OC Archaea; Euryarchaeota; Archaeoglobi; Archaeoglobales;
OC Archaeoglobaceae; Archaeoglobus.
OX NCBI_TaxID=2234;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=VC-16 / DSM 4304 / ATCC 49558;
RX MEDLINE=98049343; PubMed=9389475;
RA Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,
RA Ketchum K.A., Dodson R.J., Winn M., Hickey E.K., Peterson J.D.,
RA Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C.,

RA Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,
RA Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,
RA Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou L.,
RA Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T.,
RA Cotton M.D., Spriggs T., Artach P., Kaine B.P., Sykes S.M.,
RA Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,
RA Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
RA Venter J.C.;
RT "The complete genome sequence of the hyperthermophilic, sulphate-
reducing archaeon Archaeoglobus fulgidus.";
RL Nature 390:364-370(1997).
DR EMBL; AE000952; AAB89036.1; -.
DR PIR; H69526; H69526.
DR HSSP; P20708; 1GHJ.
DR TIGR; AF2216; -.
DR GO; GO:0009374; F:biotin binding; IEA.
DR InterPro; IPR001882; Biotin_BS.
DR InterPro; IPR000089; Biotin_lipoyl.
DR Pfam; PF00364; biotin_lipoyl; 1.
DR PROSITE; PS00188; BIOTIN; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 140 AA; 15686 MW; 30B449C45489C14A CRC64;
Query Match 52.0%; Score 178; DB 17; Length 140;
Best Local Similarity 54.7%; Pred. No. 7.5e-11;
Matches 35; Conservative 13; Mismatches 16; Indels 0; Gaps 0;
QY 4 IPAPLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTGGKVEKVLVKERDAVQGG 63
Db 74 ITAPMAGVVTKILKKVGEKVKAGETVLIIEAMKMEINPIASPEDGEIAEIVVKEGDKVASG 133
QY 64 QGLI 67
Db 134 DVLV 137
RESULT 7
O891Y8 PRELIMINARY; PRT; 986 AA.
AC O891Y8;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Pyruvate carboxylase (EC 6.4.1.1).
GN CTC02224.
OS Clostridium tetani.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1513;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Massachusetts / E88;
RX MEDLINE=22457253; PubMed=12552129;
RA Brueggemann H., Baumer S., Fricke W.F., Wierer A., Liesegang H.,
RA Decker I., Herzberg C., Martinez-Arias R., Merkl R., Henne A.,
RA Gottschalk G.;
RT "The genome sequence of Clostridium tetani, the causative agent of
tetanus disease.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:1316-1321(2003).
DR EMBL; AE015943; AAC36707.1; -.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0009374; F:biotin binding; IEA.
DR GO; GO:0016874; F:ligase activity; IEA.
DR GO; GO:0004736; F:pyruvate carboxylase activity; IEA.
DR InterPro; IPR001882; Biotin_BS.
DR InterPro; IPR000089; Biotin_lipoyl.
DR InterPro; IPR005482; CPase_L_D2.
DR InterPro; IPR005479; CPase_L_D2.
DR InterPro; IPR000891; HMGL-like.
DR InterPro; IPR003379; PYC OADA.
DR Pfam; PF02785; Biotin_carb_C; 1.
DR Pfam; PF00364; biotin_lipoyl; 1.
DR Pfam; PF02786; CPase_L_D2; 1.

DR Pfam; PF00682; HMGL-like; 1.
DR Pfam; PF02436; PYC_OADA; 1.
DR PROSITE; PS00188; BIOTIN; 1.
DR PROSITE; PS00867; CPSASE_2; 1.
KW Ligase; Complete proteome.
SQ SEQUENCE 986 AA; 110669 MW; 8825F618B0A4B219 CRC64;

Query Match 52.0%; Score 178; DB 16; Length 986;
Best Local Similarity 52.2%; Pred. No. 7e-10; Indels 0; Gaps 0;
Matches 36; Conservative 13; Mismatches 20;

QY 1 EGEIPAPLAGTVSKILVKEGDTVKGQTVLVLEAMKMETEINAPTDGKVEKVLVKERDAV 60
Db 916 KSIQIGASIPGNISKILIKEGDTVNGKGDRIAVIEAMKMETNIVSTVGKVKIFVKEQV 975

QY 61 QGGQGLIKI 69
Db 976 KVGQLIIKI 984

RESULT 8
O67484 PRELIMINARY; PRT; 655 AA.
AC O67484;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Pyruvate carboxylase C-terminal domain.
GN PYCA OR AQ_1520.
OS Aquifex aeolicus.
OC Bacteria; Aquificae; Aquificales; Aquificaceae; Aquifex.
OX NCBI_TaxID=63363;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=VF5;
RX MEDLINE=98196666; PubMed=9537320;
RA Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,
RA Graham D.E., Overbeek R., Snead M.A., Keller M., Aujay M., Huber R.,
RA Feldman R.A., Short J.M., Olson G.J., Swanson R.V.;
RT "The complete genome of the hyperthermophilic bacterium Aquifex
RT aeolicus.";
RL Nature 392:353-358(1998).
DR EMBL; AE000744; AAC07445.1; -.
DR PIR; B70432; B70432.
DR HSSP; P02905; 1BDO.
DR GO; GO:0009374; F:biotin binding; IEA.
DR GO; GO:0003824; F:catalytic activity; IEA.
DR InterPro; IPR001882; Biotin_BS.
DR InterPro; IPR000089; Biotin_lipoyl.
DR InterPro; IPR000891; HMGL-like.
DR InterPro; IPR003379; PYC_OADA.
DR Pfam; PF00364; biotin_lipoyl; 1.
DR Pfam; PF00682; HMGL-like; 1.
DR Pfam; PF02436; PYC_OADA; 1.
DR PROSITE; PS00188; BIOTIN; 1.
KW Pyruvate; Complete proteome.
SQ SEQUENCE 655 AA; 73612 MW; 2839436F6BFE05D6 CRC64;

Query Match 50.9%; Score 174; DB 16; Length 655;
Best Local Similarity 50.0%; Pred. No. 1.1e-09;
Matches 34; Conservative 13; Mismatches 21; Indels 0; Gaps 0;

QY 2 GEIPAPLAGTVSKILVKEGDTVKGQTVLVLEAMKMETEINAPTDGKVEKVLVKERDAVQ 61
Db 578 GDVTPPMGKVKILVKEGEPVQQGQTVATVEAMKMETNEVHAPIDGIVKIFAKPGDQVN 637

QY 62 GGOGLIKI 69
Db 638 PDQAIMRI 645

RESULT 9
Q9XBJ1

ID Q9XBJ1 PRELIMINARY; PRT; 984 AA.
AC Q9XBJ1;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Pyruvate carboxylase (EC 6.4.1.1) (Fragment).
GN PYCA.
OS Bacillus cereus.
OC Bacteria; Firmicutes; Bacilliales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1396;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 10987;
RX MEDLINE=99231848; PubMed=10217496;
RA Okstad O.A., Hegna I., Lindbaeck T., Rishovd A.L., Kolsto A.B.;
RT "Genome organisation is not conserved between Bacillus cereus and
RT Bacillus subtilis.";
RL Microbiology 145:621-631(1999).
DR EMBL; AJ010111; CAB40604.1; -.
DR PIR; T44608; T44608.
DR HSSP; P24182; 1DV2.
DR GO; GO:0005737; C:cytoplasm; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0016874; F:ligase activity; IEA.
DR GO; GO:0004736; F:pyruvate carboxylase activity; IEA.
DR GO; GO:0006094; P:gluconeogenesis; IEA.
DR InterPro; IPR005482; Biotin_carb_C.
DR InterPro; IPR000089; Biotin_lipoyl.
DR InterPro; IPR005479; CPase_L_D2.
DR InterPro; IPR000891; HMGL-like.
DR InterPro; IPR003379; PYC_OADA.
DR InterPro; IPR005930; Pyruv_carbox.
DR Pfam; PF02785; Biotin_carb_C; 1.
DR Pfam; PF00364; biotin_lipoyl; 1.
DR Pfam; PF02786; CPSase_L_D2; 1.
DR Pfam; PF00682; HMGL-like; 1.
DR Pfam; PF02436; PYC_OADA; 1.
DR TIGRFAMS; TIGR01235; pyruv_carbox; 1.
DR PROSITE; PS00867; CPSASE_2; 1.
KW Ligase.
FT NON TER 1
SQ SEQUENCE 984 AA; 110135 MW; 7AB52F8D453A147D CRC64;

Query Match 50.9%; Score 174; DB 2; Length 984;
Best Local Similarity 53.0%; Pred. No. 1.8e-09;
Matches 35; Conservative 13; Mismatches 18; Indels 0; Gaps 0;

QY 4 IPAPLAGTVSKILVKEGDTVKGQTVLVLEAMKMETEINAPTDGKVEKVLVKERDAVQGG 63
Db 917 ISATWPGTVIKVVKEGDEVKKGDSMAITAMKMETTVQAPFNGKVKVYVNDGDAIQTG 976

QY 64 QGLIKI 69
Db 977 DLLIEL 982

RESULT 10
Q81MT6 PRELIMINARY; PRT; 1148 AA.
ID Q81MT6
AC Q81MT6;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Pyruvate carboxylase.
GN PYC OR BA4157.
OS Bacillus anthracis (strain Ames).
OC Bacteria; Firmicutes; Bacilliales; Bacillaceae; Bacillus.
OX NCBI_TaxID=198094;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22608414; PubMed=12721629;
RA Read T.D., Peterson S.N., Tourasse N., Baillie L.W., Paulsen I.T.,
RA Nelson K.E., Tettelin H., Fouts D.E., Eisen J.A., Gill S.R.,

RA Holtzappple E.K., Okstad O.A., Helgason E., Rilstone J., Wu M.,
RA Kolonay J.F., Beanan M.J., Dodson R.J., Brinkac L.M., Gwinn M.,
RA DeBoy R.T., Madpu R., Daugherty S.C., Durkin A.S., Haft D.H.,
RA Nelson W.C., Peterson J.D., Pop M., Khouri H.M., Radune D.,
RA Benton J.L., Mahamoud Y., Jiang L., Hance I.R., Weidman J.F.,
RA Berry K.J., Plaut R.D., Wolf A.M., Watkins K.L., Nierman W.C.,
RA Hazen A., Cline R., Redmond C., Thwaiter J.E., White O., Salzberg S.L.,
RA Thomason B., Friedlander A.M., Koehler T.M., Hanna P.C., Kolsto A.-B.,
RA Fraser C.M.;
RT "The genome sequence of Bacillus anthracis Ames and comparison to
RT closely related bacteria";
RL Nature 423:81-86(2003).
DR EMBL; AE017037; AAP27881.1; --
DR TIGR; BA4157; --
DR GO; GO:0005737; C:cytoplasm; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0016874; F:ligase activity; IEA.
DR GO; GO:0004736; F:pyruvate carboxylase activity; IEA.
DR GO; GO:0006094; P:gluconeogenesis; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR005482; Biotin carb C.
DR InterPro; IPR000089; Biotin lipoyl.
DR InterPro; IPR005479; CPase_L_D2.
DR InterPro; IPR005481; CPase_L_N.
DR InterPro; IPR000891; HMGL-like.
DR InterPro; IPR003379; PYC OADA.
DR InterPro; IPR005930; Pyruv carbox.
DR Pfam; PF02785; Biotin carb C; 1.
DR Pfam; PF00364; biotin_lipoyl; 1.
DR Pfam; PF00289; CPSase_L chain; 1.
DR Pfam; PF02786; CPSase_L_D2; 1.
DR Pfam; PF00682; HMGL-like; 1.
DR Pfam; PF02436; PYC OADA; 1.
DR TIGRFAMs; TIGR01235; pyruv carbox; 1.
DR PROSITE; PS00866; CPSASE_1; 1.
DR PROSITE; PS00867; CPSASE_2; 1.
DR PROSITE; PS00867; CPSASE_2; 1.
KW Pyruvate; Complete proteome.
SQ SEQUENCE 1148 AA; 128573 MW; 57B97F8D9D1287BF CRC64;

Query Match 50.9%; Score 174; DB 16; Length 1148;
Best Local Similarity 53.0%; Pred. No. 2.2e-09;
Matches 35; Conservative 13; Mismatches 18; Indels 0; Gaps 0;

QY 4 IPAPLAGTIVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTQDKVEKVLVKERDAVQGG 63
Db 1081 ISATMPGTIVKVVVKEGDEVKKGDSMAITAMKMETTVQAPFNGKVKVYVNDGDAIQTG 1140
QY 64 QGLIKI 69
Db 1141 DLLIEL 1146

RESULT 11
Q819M9 PRELIMINARY; PRT; 1148 AA.
AC Q819M9;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Pyruvate carboxylase (EC 6.4.1.1).
GN BC3947.
OS Bacillus cereus (strain ATCC 14579 / DSM 31).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=226900;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22608415; PubMed=12721630;
RA Ivanova N., Sorokin A., Anderson I., Galleron N., Candelon B.,
RA Kapatal V., Bhattacharyya A., Reznik G., Mikhailova N., Lapidus A.,
RA Chu L., Mazur M., Goltsman E., Larsen N., D'Souza M., Walunas T.,
RA Grechkin Y., Pusch G., Haselkorn R., Fonstein M., Ehrlich S.D.,
RA Overbeek R., Kyrpides N.;
RT "Genome sequence of Bacillus cereus and comparative analysis with

RT Bacillus anthracis";
RL Nature 423:87-91(2003).
DR EMBL; AE017010; AAP10867.1; --
DR GO; GO:0005737; C:cytoplasm; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0016874; F:ligase activity; IEA.
DR GO; GO:0004736; F:pyruvate carboxylase activity; IEA.
DR GO; GO:0006094; P:gluconeogenesis; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR005482; Biotin carb C.
DR InterPro; IPR000089; Biotin lipoyl.
DR InterPro; IPR005479; CPase_L_D2.
DR InterPro; IPR005481; CPase_L_N.
DR InterPro; IPR000891; HMGL-like.
DR InterPro; IPR003379; PYC OADA.
DR InterPro; IPR005930; Pyruv carbox.
DR Pfam; PF02785; Biotin carb C; 1.
DR Pfam; PF00364; biotin_lipoyl; 1.
DR Pfam; PF00289; CPSase_L chain; 1.
DR Pfam; PF02786; CPSase_L_D2; 1.
DR Pfam; PF00682; HMGL-like; 1.
DR Pfam; PF02436; PYC OADA; 1.
DR TIGRFAMs; TIGR01235; pyruv carbox; 1.
DR PROSITE; PS00866; CPSASE_1; 1.
DR PROSITE; PS00867; CPSASE_2; 1.
KW Ligase; Pyruvate; Complete proteome.
SQ SEQUENCE 1148 AA; 128442 MW; EE5CC5BA99D8E191 CRC64;

Query Match 50.9%; Score 174; DB 16; Length 1148;
Best Local Similarity 53.0%; Pred. No. 2.2e-09;
Matches 35; Conservative 13; Mismatches 18; Indels 0; Gaps 0;

QY 4 IPAPLAGTIVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTQDKVEKVLVKERDAVQGG 63
Db 1081 ISATMPGTIVKVVVKEGDEVKKGDSMAITAMKMETTVQAPFNGKVKVYVNDGDAIQTG 1140
QY 64 QGLIKI 69
Db 1141 DLLIEL 1146

RESULT 12
Q97VY7 PRELIMINARY; PRT; 186 AA.
ID Q97VY7
AC Q97VY7;
DT 01-OCT-2001 (TREMBlrel. 18, Created)
DT 01-OCT-2001 (TREMBlrel. 18, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Biotin carboxyl carrier protein of propionyl-CoA carboxylase beta
DE subunit (EC 6.4.1.3).
GN SS02464.
OS Sulfolobus solfataricus.
OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
OC Sulfolobus.
OX NCBI_TaxID=2287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 35092 / DSM 1617 / P2;
RX MEDLINE=21332296; PubMed=11427726;
RA She Q., Singh R.K., Confalonieri F., Zivanovic Y., Allard G.,
RA Awayez M.J., Chan-Weiher C.C.-Y., Clausen I.G., Curtis B.A.,
RA De Moors A., Erauso G., Fletcher C., Gordon P.M.K.,
RA Heikamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., Peng X.,
RA Thi-Ngoc H.P., Redder P., Schenk M.E., Theriault C., Tolstrup N.,
RA Charlebois R.L., Doolittle W.F., Duguet M., Gaasterland T.,
RA Garrett R.A., Ragan M.A., Sengen C.W., Van der Oost J.;
RT "The complete genome of the crenarchaeon Sulfolobus solfataricus P2";
RL Proc. Natl. Acad. Sci. U.S.A. 98:7835-7840(2001).
DR EMBL; AE006845; AAK42603.1; --
DR PIR; D90418; D90418.
DR GO; GO:0009374; F:biotin binding; IEA.
DR GO; GO:0016874; F:ligase activity; IEA.
DR GO; GO:0004658; F:propionyl-CoA carboxylase activity; IEA.

DR InterPro; IPR001882; Biotin_BS.
DR InterPro; IPR000089; Biotin_lipoyl.
DR Pfam; PF00364; biotin_lipoyl; 1.
DR PROSITE; PS00188; BIOTIN; 1.
KW Ligase; Complete proteome.
SQ SEQUENCE 186 AA; 21166 MW; DB26587C39883B08 CRC64;

Query Match 49.7%; Score 170; DB 17; Length 186;
Best Local Similarity 55.1%; Pred. No. 7e-10;
Matches 38; Conservative 9; Mismatches 22; Indels 0; Gaps 0;

QY 1 EGEIPAPLAGTVSKILVKEGDTVKGQTVLVLEAMKMETEINAPTQKVEKVLVKERDAV 60
Db 117 EGEIVSPLFGRVVKIRVKEGDAVNGKQPLLSIEAMKAETVISSPIGGIVQKILKEGGV 176

QY 61 QGGQGLIKI 69
Db 177 KKGDIILIVI 185

RESULT 13
Q9WZH6 PRELIMINARY; PRT; 134 AA.
AC Q9WZH6;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Propionyl-CoA carboxylase, gamma subunit.
GN TM0717.
OS Thermotoga maritima.
OC Bacteria; Thermotogae; Thermotogales; Thermotogaceae; Thermotoga.
OX NCBI_TaxID=2336;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NSB8 / DSM 3109;
RX MEDLINE=99287316; PubMed=10360571;
RA Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,
Raft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,
Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,
Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,
Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;
RT "Evidence for lateral gene transfer between Archaea and Bacteria from
genome sequence of Thermotoga maritima."
RL Nature 399:323-329(1999).
DR EMBL; AB001743; AAD35799.1; -.
DR PIR; C72341; C72341.
DR HSSP; P02905; 1BDO.
DR TIGR; TM0717; -.
DR InterPro; IPR000089; Biotin_lipoyl.
DR Pfam; PF00364; biotin_lipoyl; 1.
KW Complete proteome.
SQ SEQUENCE 134 AA; 15131 MW; A3BFBAACE8574BC1 CRC64;

Query Match 48.8%; Score 167; DB 16; Length 134;
Best Local Similarity 51.5%; Pred. No. 9.9e-10;
Matches 34; Conservative 12; Mismatches 20; Indels 0; Gaps 0;

QY 4 IPAPLAGTVSKILVKEGDTVKGQTVLVLEAMKMETEINAPTQKVEKVLVKERDAVQGG 63
Db 68 VKAPMAGIVLVKEGQKVNVDKLLVFEAMKMENELQSEFSGTVKEILVKEGDNIEGT 127

QY 64 QGLIKI 69
Db 128 QILMKI 133

RESULT 14
Q48826 PRELIMINARY; PRT; 596 AA.
ID Q48826
AC Q48826;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Oxaloacetate decarboxylase alpha-chain.
GN OADA.
OS Legionella pneumophila.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Legionellales;
OC Legionellaceae; Legionella.
OX NCBI_TaxID=446;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Corby;
RX MEDLINE=97120897; PubMed=8961567;
RA Jain B., Brand B.C., Lueck P.C., Di Bevardino M., Dimroth P.,
Hacker J.;
RT "An oxaloacetate decarboxylase homologue protein influences the
intracellular survival of Legionella pneumophila.";
RL FEMS Microbiol. Lett. 145:273-279(1996).
CC -I- COFACTOR: BIOTIN (BY SIMILARITY).
DR EMBL; X99678; CAA67994.1; -.
DR HSSP; P11961; 1LAB.
DR GO; GO:0009374; F:biotin binding; IEA.
DR GO; GO:0003824; F:catalytic activity; IEA.
DR GO; GO:0008948; F:oxaloacetate decarboxylase activity; IEA.
DR GO; GO:0006520; P:amino acid metabolism; IEA.
DR GO; GO:0006814; P:sodium ion transport; IEA.
DR InterPro; IPR001882; Biotin_BS.
DR InterPro; IPR000089; Biotin_lipoyl.
DR InterPro; IPR000891; HMGL-like.
DR InterPro; IPR005776; Oada.
DR InterPro; IPR003379; PYC_OADA.
DR InterPro; IPR000634; S/T dehydratase_BS.
DR Pfam; PF00364; biotin_lipoyl; 1.
DR Pfam; PF00682; HMGL-like; 1.
DR Pfam; PF02436; PYC_OADA; 1.
DR TIGRFAMS; TIGR01108; oada; 1.
DR PROSITE; PS00188; BIOTIN; 1.
DR PROSITE; PS00165; DEHYDRATASE_SER_THR; 1.
KW Biotin.
SQ SEQUENCE 596 AA; 65667 MW; 55DBEAF96919C86 CRC64;

Query Match 48.8%; Score 167; DB 2; Length 596;
Best Local Similarity 51.5%; Pred. No. 5.5e-09;
Matches 35; Conservative 12; Mismatches 21; Indels 0; Gaps 0;

QY 2 GEIPAPLAGTVSKILVKEGDTVKGQTVLVLEAMKMETEINAPTQKVEKVLVKERDAVQ 61
Db 526 GDITVAIPGSIHIVSAGDEVKAGQAVLVIEAMKMETEIKAPANGVVABILCQKGDKVT 585

QY 62 GGQGLIKI 69
Db 586 PGQVLIRV 593

RESULT 15
Q97FR7 PRELIMINARY; PRT; 1144 AA.
AC Q97FR7;
DT 01-OCT-2001 (TrEMBLrel. 18, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Pyruvate carboxylase, PYKA.
GN CAC2660.
OS Clostridium acetobutylicum.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1488;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 824 / DSM 792 / VKM B-1787;
RX MEDLINE=21359325; PubMed=11466286;
RA Noelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q.,
Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I.,
Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J.,
Bennett G.N., Koonin E.V., Smith D.R.;

RT "Genome sequence and comparative analysis of the solvent-producing
RT bacterium Clostridium acetobutylicum.";
RL J. Bacteriol. 183:4823-4838(2001).
DR EMBL; AE007763; AAK80607.1; -.
DR PIR; D97227; D97227.

DR GO; GO:0005737; C:cytoplasm; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0009374; F:biotin binding; IEA.
DR GO; GO:0004086; F:carbamoyl-phosphate synthase activity; IEA.
DR GO; GO:0016874; F:ligase activity; IEA.
DR GO; GO:0004736; F:pyruvate carboxylase activity; IEA.
DR GO; GO:0006094; P:gluconeogenesis; IEA.
DR GO; GO:0008152; P:metabolism; IEA.

DR InterPro; IPR001882; Biotin_BS.
DR InterPro; IPR005482; Biotin_carb_C.
DR InterPro; IPR000089; Biotin_lipoyl.
DR InterPro; IPR005483; CPase_L.
DR InterPro; IPR005479; CPase_L_D2.
DR InterPro; IPR005481; CPase_L_N.
DR InterPro; IPR000891; HMGL-like.
DR InterPro; IPR003379; PYC_OADA.

DR InterPro; IPR005930; Pyruv_carbox.
DR Pfam; PF02785; Biotin_carb_C; 1.
DR Pfam; PF00364; biotin_lipoyl; 1.
DR Pfam; PF00289; CPSase_L_chain; 1.
DR Pfam; PF02786; CPSase_L_D2; 1.
DR Pfam; PF00682; HMGL-like; 1.
DR Pfam; PF02436; PYC_OADA; 1.
DR PRINTS; PR00098; CPSASE.

DR TIGRFAMS; TIGR01235; pyruv carbox; 1.
DR PROSITE; PS00188; BIOTIN; 1.
DR PROSITE; PS00866; CPSASE_1; 1.
DR PROSITE; PS00867; CPSASE_2; 1.
KW Complete proteome.
SQ SEQUENCE 1144 AA; 127709 MW; 519FA29A8008F326 CRC64;

Query Match 48.8%; Score 167; DB 16; Length 1144;
Best Local Similarity 50.7%; Pred. No. 1.2e-08;
Matches 34; Conservative 11; Mismatches 22; Indels 0; Gaps 0;

QY 3 EIPAPLAGTIVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVLVVKERDAVQG 62
Db 1077 EIGASIPGNVVKVPGDKVKKGSLSLVLEAMKMETNVSVDGTVGGIFVKEGQVQS 1136

QY 63 GQGGLIKI 69
Db 1137 GQLLVKL 1143

RESULT 16
Q8J2Z3 ID Q8J2Z3 PRELIMINARY; PRT; 167 AA.
AC Q8J2Z3;
DT 01-MAR-2003 (TReMBLrel. 23, Created)
DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Biotin carrier protein.
GN ACCB.

OS Metallosphaera sedula.
OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
OC Metallosphaera.
OX NCBI_TaxID=43687;
RN [1]

SEQUENCE FROM N.A.
RA Hugler M., Krieger R.S., Jahn M., Fuchs G.;
RT "Characterization of Acetyl-CoA/Propionyl-CoA Carboxylase in
RT Metallosphaera sedula - Carboxylating Enzyme in the 3-
RT Hydroxypropionate Cycle for Autotrophic Carbon Fixation.";
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF461116; AA015573.1; -.
DR InterPro; IPR000089; Biotin_lipoyl.
DR Pfam; PF00364; biotin_lipoyl; 1.
SQ SEQUENCE 167 AA; 18634 MW; FC4504CE2EE7D91C CRC64;

Query Match 48.2%; Score 165; DB 1; Length 167;
Best Local Similarity 52.2%; Pred. No. 2.1e-09;
Matches 36; Conservative 10; Mismatches 23; Indels 0; Gaps 0;
QY 1 EGEIPAPLAGTIVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVLVVKERDAV 60
Db 98 EGEVLSPLQGRVVQVRVKEGDVAVNKGQPLLSIEAMKSETIVSAPISGLVKEKVLVVKAGQGV 157
QY 61 QGGQGLIKI 69
Db 158 KKGDIILVVI 166

RESULT 17
Q88VCS ID Q88VCS PRELIMINARY; PRT; 1144 AA.
AC Q88VCS;
DT 01-JUN-2003 (TReMBLrel. 24, Created)
DT 01-JUN-2003 (TReMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Pyruvate carboxylase (EC 6.4.1.1).
GN PYCA OR LP 2136.
OS Lactobacillus plantarum.
OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
OC Lactobacillus.
OX NCBI_TaxID=1590;
RN [1]

SEQUENCE FROM N.A.
RC STRAIN=NCIMB 8826 / WCFS1;
RX MEDLINE=22480296; PubMed=12566566;
RA Kleerebezem M., Boekhorst J., van Kranenburg R., Molenaar D.,
RA Kuipers O.P., Leer R., Tarchini R., Peters S.A., Sandbrink H.M.,
RA Fiers M.W.E.J., Stiekema W., Klein Lankhorst R.M., Bron P.A.,
RA Hoffer S.M., Nierop Groot M.N., Kerkhoven R., De Vries M., Ursing B.,
RA De Vos W.M., Siezen R.J.;

RT "Complete genome sequence of Lactobacillus plantarum WCFS1.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:1990-1995(2003).
DR EMBL; AL935258; CAD64497.1; -.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0008716; P:D-alanine-D-alanine ligase activity; IEA.
DR GO; GO:0016874; F:ligase activity; IEA.
DR GO; GO:0004736; F:pyruvate carboxylase activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.

DR InterPro; IPR005482; Biotin_carb_C.
DR InterPro; IPR000089; Biotin_lipoyl.
DR InterPro; IPR005479; CPase_L_D2.
DR InterPro; IPR005481; CPase_L_N.
DR InterPro; IPR000291; Dala_lig_Van.
DR InterPro; IPR000891; HMGL-like.
DR InterPro; IPR003379; PYC_OADA.
DR Pfam; PF02785; Biotin_carb_C; 1.
DR Pfam; PF00364; biotin_lipoyl; 1.
DR Pfam; PF00289; CPSase_L_chain; 1.
DR Pfam; PF02786; CPSase_L_D2; 1.
DR Pfam; PF01820; Dala_Dala_ligas; 1.
DR Pfam; PF00682; HMGL-like; 1.
DR Pfam; PF02436; PYC_OADA; 1.
DR PROSITE; PS00866; CPSASE_1; 1.
DR PROSITE; PS00867; CPSASE_2; 1.
KW Ligase; Complete proteome.
SQ SEQUENCE 1144 AA; 127299 MW; BFAPA8AD6325DCDF CRC64;

Query Match 48.2%; Score 165; DB 16; Length 1144;
Best Local Similarity 49.3%; Pred. No. 1.9e-08;
Matches 34; Conservative 13; Mismatches 22; Indels 0; Gaps 0;
QY 1 EGEIPAPLAGTIVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVLVVKERDAV 60
Db 1073 EDEVGATMSGSVLKLVLKKGQTVKKGEPLLVTEAMKMETTIOAPEDGVIEHIYVNAQDVI 1132
QY 61 QGGQGLIKI 69


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Db 507 EGEMTAPVSGTLQSPKVDGETVSEGDLLAVMEAMKMETQIVATRACKV-RLIVKEGDYL 565
QY 61 QGGQGLIKI 69
Db 566 QAGATLIDI 574

RESULT 23
Q8A737 PRELIMINARY; PRT; 144 AA.
AC Q8A737;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Biotin carboxyl carrier protein (BCCP).
GN BT1688.
OS Bacteroides thetaiotaomicron.
OC Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
OC Bacteroidaceae; Bacteroides.
OX NCBI_TaxID=818;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=VPI-5482 / ATCC 29148;
RX MEDLINE=22550858; PubMed=12663928;
RA Xu J., Bjursell M.K., Himrod J., Deng S., Carmichael L.K.,
RA Chiang H.C., Hooper L.V., Gordon J.I.;
RT "A genomic view of the human-Bacteroides thetaiotaomicron symbiosis.";
RL Science 299:2074-2076(2003).
DR EMBL; AE016932; AAC076795.1; -.
DR GO; GO:0009317; C:acetyl-CoA carboxylase complex; IEA.
DR GO; GO:0003989; F:acetyl-CoA carboxylase activity; IEA.
DR GO; GO:0009374; F:biotin binding; IEA.
DR GO; GO:0006633; P:fatty acid biosynthesis; IEA.
DR InterPro; IPR001249; AcCoA biotinCC.
DR InterPro; IPR001882; Biotin_BS.
DR InterPro; IPR000089; Biotin_lipoyl.
DR Pfam; PF00364; biotin_lipoyl; 1.
DR PRINTS; PR01071; ACOABTIOTINCC.
DR PROSITE; PS00188; BIOTIN; 1.
KW Complete proteome.
SQ SEQUENCE 144 AA; 15487 MW; 462383E2FB85601E CRC64;

Query Match 46.5%; Score 159; DB 16; Length 144;
Best Local Similarity 50.0%; Pred. No. 7.3e-09;
Matches 33; Conservative 10; Mismatches 23; Indels 0; Gaps 0;

QY 4 IPAPLAGTVSKILVKEGDTVKGQTVLVLEAMKMETEINAPTDGKVKVLERDAVQGG 63
Db 78 VKSPLPGVILDIKVNVDGTVKRGQTIILLEAMKMENNINADKDGKVTAINVNGDSVLEG 137
QY 64 QGLIKI 69
Db 138 NDLVII 143

RESULT 24
Q88C37 PRELIMINARY; PRT; 602 AA.
AC Q88C37;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Oxaloacetate decarboxylase, alpha subunit.
GN OADA OR PP5346.
OS Pseudomonas putida (strain KT2440).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=160488;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22423060; PubMed=12534463;
RA Nelson K.E., Weinel C., Paulsen I.T., Dodson R.J., Hilbert H.,
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RA Martins dos Santos V.A.P., Fouts D.E., Gill S.R., Pop M., Holmes M.,
RA Brinkac L., Beanan M., DeBoy R.T., Daugherty S., Kolonay J.,
RA Madupu R., Nelson W., White O., Peterson J., Khouri H., Hance I.,
RA Chris Lee P., Holtzapple E., Scanlan D., Tran K., Moazzez A.,
RA Utterback T., Rizzo M., Lee K., Kosack D., Moestl D., Wedler H.,
RA Lauber J., Stjepandic D., Hoheisel J., Straetz M., Heim S.,
RA Kiewitz C., Eisen J., Timmis K.N., Duesterhoeft A., Tuemmler B.,
RA Fraser C.M.;
RT "Complete genome sequence and comparative analysis of the
RT metabolically versatile Pseudomonas putida KT2440.";
RL Environ. Microbiol. 4:799-808(2002).
DR EMBL; AE016794; AAN70911.1; -.
DR TIGR; PP5346; -.
DR GO; GO:0003824; F:catalytic activity; IEA.
DR GO; GO:0006520; P:amino acid metabolism; IEA.
DR InterPro; IPR000089; Biotin_lipoyl.
DR InterPro; IPR000891; HMGL-like.
DR InterPro; IPR003379; PYC OADA.
DR InterPro; IPR000634; S/T_dehydratse_BS.
DR Pfam; PF00364; biotin_lipoyl; 1.
DR Pfam; PF00682; HMGL-like; 1.
DR Pfam; PF02436; PYC OADA; 1.
DR PROSITE; PS00165; DEHYDRATASE_SER_THR; 1.
KW Complete proteome.
SQ SEQUENCE 602 AA; 65626 MW; 98552963F0E691A7 CRC64;

Query Match 46.5%; Score 159; DB 16; Length 602;
Best Local Similarity 50.0%; Pred. No. 3.8e-08;
Matches 34; Conservative 10; Mismatches 24; Indels 0; Gaps 0;

QY 2 GEIPAPLAGTVSKILVKEGDTVKGQTVLVLEAMKMETEINAPTDGKVKVLERDAVQ 61
Db 533 GHVSTTMPGNIVDLVKEGDMVKAGQAVLITEAMKMETEVQAAIAGKVVAIHVAKGDRVT 592
QY 62 GGQGLIKI 69
Db 593 PGEILIEI 600

RESULT 25
Q92H13 PRELIMINARY; PRT; 665 AA.
AC Q92H13;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Propionyl-CoA carboxylase alpha chain.
GN PCCA OR RC0959.
OS Rickettsia conorii.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
OC Rickettsiaceae; Rickettsieae; Rickettsia.
OX NCBI_TaxID=781;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Malish 7;
RX MEDLINE=21442074; PubMed=11557893;
RA Ogata H., Audic S., Renesto-Audiffren P., Fournier P.-E., Barbe V.,
RA Samson D., Roux V., Cossart P., Weissenbach J., Claverie J.-M.,
RA Raoult D.;
RT "Mechanisms of evolution in Rickettsia conorii and R. prowazekii.";
RL Science 293:2093-2098(2001).
DR EMBL; AE008649; AAL03497.1; -.
DR PIR; G97819; G97819.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0009374; F:biotin binding; IEA.
DR GO; GO:0016874; F:ligase activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR001882; Biotin_BS.
DR InterPro; IPR005482; Biotin_carb_C.
DR InterPro; IPR000089; Biotin_lipoyl.
DR InterPro; IPR005479; CPase_L_D2.
DR InterPro; IPR005481; CPase_L_N.
DR Pfam; PF02785; Biotin_carb_C; 1.
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DR Pfam; PF00364; biotin lipoyl; 1.
DR Pfam; PF00289; CPSase_L_chain; 1.
DR Pfam; PF02786; CPSase_L_D2; 1.
DR PROSITE; PS00188; BIOTIN; 1.
DR PROSITE; PS00866; CPSASE_1; 1.
DR PROSITE; PS00867; CPSASE_2; 1.
KW Complete proteome.
SQ SEQUENCE 665 AA; 73320 MW; 3054C1E18E0C14A3 CRC64;

Query Match 46.5%; Score 159; DB 16; Length 665;
Best Local Similarity 50.0%; Pred. No. 4.2e-08;
Matches 33; Conservative 12; Mismatches 21; Indels 0; Gaps 0;

QY 3 EIPAPLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVLVKERDAVQ 62
Db ELQAPLSGQIAAIKVKEGQVTAQGEIMILTAMKMNILIAERDGIKFIKFNKDNVIR 657

QY 63 GQGLIK 68
Db GQVLE 663

RESULT 26
Q974R8 PRELIMINARY; PRT; 169 AA.
AC Q974R8;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Putative biotin carboxyl carrier protein.
GN ST0592.
OS Sulfolobus tokodaii.
OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
OC Sulfolobus.
OX NCBI_TaxID=111955;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=JCM 10545 / 7;
RX MEDLINE=21456156; PubMed=11572479;
RA Kawarabayasi Y., Hino Y., Horikawa H., Jin-no K., Takahashi M.,
RA Sekine M., Baba S.-I., Ankai A., Kosugi H., Hosoyama A., Fukui S.,
RA Nagai Y., Nishijima K., Otsuka R., Nakazawa H., Takamiya M., Kato Y.,
RA Yoshizawa T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A.,
RA Aoki K.-I., Masuda S., Yanagii M., Nishimura M., Yamagishi A.,
RA Oshima T., Kikuchi H.;
RT "Complete genome sequence of an aerobic thermoacidophilic
RT Crenarchaeon, Sulfolobus tokodaii strain7.";
RL DNA Res. 8:123-140(2001).
DR EMBL; AP000983; BAB65589.1; -;
DR InterPro; IPR000089; Biotin lipoyl.
DR Pfam; PF00364; biotin lipoyl; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 169 AA; 18839 MW; 4F1D96761F5BE3DD CRC64;

Query Match 46.2%; Score 158; DB 17; Length 169;
Best Local Similarity 49.3%; Pred. No. 1.1e-08;
Matches 34; Conservative 12; Mismatches 23; Indels 0; Gaps 0;

QY 1 EGEIPAPLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVLVKERDAV 60
Db EGEILSPMQGRIVQIRVKEGDAVNKGQPLLSIEAMKSETVISAPVGGVQKIMVKPGQGV 159

QY 61 QGGGLIKI 69
Db KKGDLILLI 168

RESULT 27
Q9HTD1 PRELIMINARY; PRT; 607 AA.
ID Q9HTD1
AC Q9HTD1;
DT 01-MAR-2001 (TReMBLrel. 16, Created)
DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)

DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Probable transcarboxylase subunit.
GN PA5435.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 15692 / PA01;
RX MEDLINE=20437337; PubMed=10984043;
RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warren P.,
RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
RA Garber R.L., Goltry L., Tolentino E., Westbrook-Wadman S., Yuan Y.,
RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;
RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an
RT opportunistic pathogen.";
RL Nature 406:959-964(2000).
DR EMBL; AE004956; AAG08820.1; -;
DR PIR; F82966; F82966.
DR HSSP; P02905; 3BDO.
DR GO; GO:0003824; F:catalytic activity; IEA.
DR GO; GO:0008948; F:oxaloacetate decarboxylase activity; IEA.
DR GO; GO:0006520; P:amino acid metabolism; IEA.
DR GO; GO:0006814; P:sodium ion transport; IEA.
DR InterPro; IPR000089; Biotin lipoyl.
DR InterPro; IPR000891; HMGL-like.
DR InterPro; IPR005776; Oada.
DR InterPro; IPR003379; PYC OADA.
DR InterPro; IPR000634; S/T_dehydrtse_BS.
DR Pfam; PF00364; biotin lipoyl; 1.
DR Pfam; PF00682; HMGL-like; 1.
DR Pfam; PF02436; PYC OADA; 1.
DR TIGRFAMs; TIGR01108; oada; 1.
DR PROSITE; PS00165; DEHYDRATASE_SER_THR; 1.
KW Complete proteome.
SQ SEQUENCE 607 AA; 66095 MW; 232AB0E9B935E010 CRC64;

Query Match 46.2%; Score 158; DB 16; Length 607;
Best Local Similarity 48.5%; Pred. No. 4.8e-08;
Matches 33; Conservative 12; Mismatches 23; Indels 0; Gaps 0;

QY 2 GEIPAPLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVLVKERDAVQ 61
Db GHVSTTPGNIVDVLVKEGDSVKAGQAVLITEAMKMETEVQAGIAGTVKAIHVAKGDRVN 597

QY 62 GQGLIKI 69
Db PGEILLIEI 605

RESULT 28
Q92CW1 PRELIMINARY; PRT; 1146 AA.
ID Q92CW1
AC Q92CW1;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Pyca protein.
GN PYCA OR LIN1060.
OC Listeria innocua.
OC Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
OX NCBI_TaxID=1642;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CLIP 11262 / Serovar 6a;
RX MEDLINE=21537279; PubMed=11679669;
RA Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,
RA Baquero F., Berche P., Bloeker H., Brandt P., Chakraborty T.,
RA Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,
RA Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,

RA Entian K.-D., Fsihi H., Garcia-del Portillo F., Garrido P.,
RA Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
RA Jones L.-M., Kaerst U., Krefit J., Kuhn M., Kunst F., Kurapkat G.,
RA Madoeno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,
RA Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
RA Remmel B., Rose M., Schluter T., Simoes N., Tierrez A.,
RA Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.,
RA "Comparative genomics of *Listeria species*.",
RA Science 294:849-852(2001).
RA EMBL; AL59167; CAC96291.1; -.
RA PIR; AC1565; AC1565.
RA ListList; LMO1060; -.
RA GO; GO:0005737; C:cytoplasm; IEA.
RA GO; GO:0005524; F:ATP binding; IEA.
RA GO; GO:0016874; F:ligase activity; IEA.
RA GO; GO:0004736; F:pyruvate carboxylase activity; IEA.
RA GO; GO:0006094; P:gluconeogenesis; IEA.
RA GO; GO:0008152; P:metabolism; IEA.
RA InterPro; IPR005482; Biotin carb C.
RA InterPro; IPR000089; Biotin_lipoyl.
RA InterPro; IPR005479; CPase_L_D2.
RA InterPro; IPR005481; CPase_L_N.
RA InterPro; IPR000891; HMGL-like.
RA InterPro; IPR003379; PYC_OADA.
RA InterPro; IPR005930; Pyruv carbox.
RA Pfam; PF02785; Biotin carb_C; 1.
RA Pfam; PF00364; biotin_lipoyl; 1.
RA Pfam; PF00289; CPSase_L_chain; 1.
RA Pfam; PF02786; CPSase_L_D2; 1.
RA Pfam; PF00682; HMGL-like; 1.
RA Pfam; PF02436; PYC_OADA; 1.
RA TIGRFAMs; TIGR01235; pyruv carbox; 1.
RA PROSITE; PS00866; CPSASE_1; 1.
RA PROSITE; PS00867; CPSASE_2; 1.
KW Complete proteome.
SQ SEQUENCE 1146 AA; 128035 MW; 3E23FFB4A289C60F CRC64;

Query Match 45.9%; Score 157; DB 16; Length 1146;
Best Local Similarity 43.9%; Pred. No. 1.3e-07;
Matches 29; Conservative 17; Mismatches 20; Indels 0; Gaps 0;

QY 4 IPAPLAGTVSKILVKEGDTVKGQTVLVLEAMKMETEINAPTQKVEKLVKRDVQGG 63
Db 1078 VGATMTGSGVIQVVVKGDSVKKGDPDLLITEAMKMETTIQAPFDGEVSSIVSDGDTIESG 1137

QY 64 QGLIKI 69
Db 1138 DLLIEV 1143

RESULT 29
QY846 PRELIMINARY; PRT; 1146 AA.
AC QY846;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE PYCA protein.
GN PYCA OR LMO1072.
OS Listeria monocytogenes.
OC Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
OX NCBI_TaxID=1639;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=EGD-e / Serovar 1/2a;
RX MEDLINE=21537279; PubMed=11679669;
RA Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,
RA Baquero F., Berche P., Bloeker H., Brandt P., Chakraborty T.,
RA Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,
RA Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
RA Entian K.-D., Fsihi H., Garcia-del Portillo F., Garrido P.,
RA Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
RA Jones L.-M., Kaerst U., Krefit J., Kuhn M., Kunst F., Kurapkat G.,

RA Madoeno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,
RA Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
RA Remmel B., Rose M., Schluter T., Simoes N., Tierrez A.,
RA Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.,
RA "Comparative genomics of *Listeria species*.",
RA Science 294:849-852(2001).
RA EMBL; AL59167; CAC99150.1; -.
RA PIR; AH1208; AH1208.
RA ListList; LMO01072; -.
RA GO; GO:0005737; C:cytoplasm; IEA.
RA GO; GO:0005524; F:ATP binding; IEA.
RA GO; GO:0016874; F:ligase activity; IEA.
RA GO; GO:0004736; F:pyruvate carboxylase activity; IEA.
RA GO; GO:0006094; P:gluconeogenesis; IEA.
RA GO; GO:0008152; P:metabolism; IEA.
RA InterPro; IPR005482; Biotin carb C.
RA InterPro; IPR000089; Biotin_lipoyl.
RA InterPro; IPR005479; CPase_L_D2.
RA InterPro; IPR005481; CPase_L_N.
RA InterPro; IPR000891; HMGL-like.
RA InterPro; IPR003379; PYC_OADA.
RA InterPro; IPR005930; Pyruv carbox.
RA Pfam; PF02785; Biotin carb_C; 1.
RA Pfam; PF00364; biotin_lipoyl; 1.
RA Pfam; PF00289; CPSase_L_chain; 1.
RA Pfam; PF02786; CPSase_L_D2; 1.
RA Pfam; PF00682; HMGL-like; 1.
RA Pfam; PF02436; PYC_OADA; 1.
RA TIGRFAMs; TIGR01235; pyruv carbox; 1.
RA PROSITE; PS00866; CPSASE_1; 1.
RA PROSITE; PS00867; CPSASE_2; 1.
KW Complete proteome.
SQ SEQUENCE 1146 AA; 128049 MW; A062F88C9A092B6F CRC64;

Query Match 45.9%; Score 157; DB 16; Length 1146;
Best Local Similarity 43.9%; Pred. No. 1.3e-07;
Matches 29; Conservative 17; Mismatches 20; Indels 0; Gaps 0;

QY 4 IPAPLAGTVSKILVKEGDTVKGQTVLVLEAMKMETEINAPTQKVEKLVKRDVQGG 63
Db 1078 VGATMTGSGVIQVVVKGDSVKKGDPDLLITEAMKMETTIQAPFDGEVSSIVSDGDTIESG 1137

QY 64 QGLIKI 69
Db 1138 DLLIEV 1143

RESULT 30
QY846 PRELIMINARY; PRT; 1150 AA.
AC QY846;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Pyruvate carboxylase.
GN PYCA OR BH2625.
OS Bacillus halodurans.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=86665;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C-125 / JCM 9153;
RX MEDLINE=20512582; PubMed=11058132;
RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
RA Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
RA Horikoshi K.;
RA "Complete genome sequence of the alkaliphilic bacterium *Bacillus*
RA halodurans and genomic sequence comparison with *Bacillus subtilis*.";
RA Nucleic Acids Res. 28:4317-4331(2000).
RA EMBL; AP001516; BAB06344.1; -.
RA PIR; A83978; A83978.
RA HSSP; P24182; 1BNC.
RA GO; GO:0005737; C:cytoplasm; IEA.

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DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0016874; F:Ligase activity; IEA.
DR GO; GO:0004736; F:pyruvate carboxylase activity; IEA.
DR GO; GO:0006094; P:gluconeogenesis; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR000152; P:metabolism; IEA.
DR InterPro; IPR000089; Biotin_lipoyl.
DR InterPro; IPR005482; Biotin_carb_C.
DR InterPro; IPR005479; CPase_L_D2.
DR InterPro; IPR005481; CPase_L_N.
DR InterPro; IPR000891; HMGL-Like.
DR InterPro; IPR003379; PYC_OADA.
DR InterPro; IPR005930; Pyruv_carbox.
DR Pfam; PF02785; Biotin_carb_C; 1.
DR Pfam; PF00364; biotin_lipoyl; 1.
DR Pfam; PF00289; CPSase_L_chain; 1.
DR Pfam; PF02786; CPSase_L_D2; 1.
DR Pfam; PF00682; HMGL-Like; 1.
DR Pfam; PF02436; PYC_OADA; 1.
DR TIGRFAMS; TIGR01235; pyruv_carbox; 1.
DR PROSITE; PS00867; CPSASE_2; 1.
KW Complete proteome.
SQ SEQUENCE 1150 AA; 128858 MW; ED6788BE8A9F3BD4 CRC64;

Query Match 45.9%; Score 157; DB 16; Length 1150;
Best Local Similarity 50.0%; Pred. No. 1.3e-07;
Matches 33; Conservative 13; Mismatches 20; Indels 0; Gaps 0;

QY 4 IPAPLAGTVSKILVKEGDTVKGQTVLVLEAMKMETEINAPTDGKVEKVLVKERDAVQGG 63
Db 1082 IGASMPGTVVKALVEKGVKQGDHLMITEAMKMETTVQAPFDGEVVALHVKGDAIQTG 1141
QY 64 QGLIKI 69
Db 1142 DLLIEV 1147

RESULT 31
Q8L2G4
ID Q8L2G4 PRELIMINARY; PRT; 1140 AA.
AC Q8L2G4;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Pyruvate carboxylase.
GN PYC.
OS Corynebacterium crenatum.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Corynebacteriaceae; Corynebacterium.
OX NCBI_TaxID=168810;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CD945;
RA Wang J., Ding J., Liu Y.;
RT "Cloning and Expression of Pyruvate Carboxylase Gene in Corynebacterium crenatum CD945."
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF503915; AAM27458.1; -.
DR GO; GO:0005737; C:cytoplasm; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0009374; F:biotin binding; IEA.
DR GO; GO:0016874; F:ligase activity; IEA.
DR GO; GO:0004736; F:pyruvate carboxylase activity; IEA.
DR GO; GO:0006094; P:gluconeogenesis; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR001882; Biotin_BS.
DR InterPro; IPR005482; Biotin_carb_C.
DR InterPro; IPR000089; Biotin_lipoyl.
DR InterPro; IPR005479; CPase_L_D2.
DR InterPro; IPR005481; CPase_L_N.
DR InterPro; IPR000891; HMGL-Like.
DR InterPro; IPR003379; PYC_OADA.
DR InterPro; IPR005930; Pyruv_carbox.
DR Pfam; PF02785; Biotin_carb_C; 1.
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DR Pfam; PF00364; biotin_lipoyl; 1.
DR Pfam; PF00289; CPSase_L_chain; 1.
DR Pfam; PF02786; CPSase_L_D2; 1.
DR Pfam; PF00682; HMGL-Like; 1.
DR Pfam; PF02436; PYC_OADA; 1.
DR TIGRFAMS; TIGR01235; pyruv_carbox; 1.
DR PROSITE; PS00188; BIOTIN; 1.
DR PROSITE; PS00867; CPSASE_2; 1.
SQ SEQUENCE 1140 AA; 123126 MW; FFA90BB7644C910E CRC64;

Query Match 45.8%; Score 156.5; DB 2; Length 1140;
Best Local Similarity 46.4%; Pred. No. 1.4e-07;
Matches 32; Conservative 13; Mismatches 23; Indels 1; Gaps 1;

QY 1 EGEIPAPLAGTVSKILVKEGDTVKGQTVLVLEAMKMETEINAPTDGKVEKVLVKERDAV 60
Db 1072 KGHVAAPFAGVVT-VTVAEQDEVKAGDAVAIEAMKMEATITASVDGKIDRVVVPAAATKV 1130
QY 61 QGGQGLIKI 69
Db 1131 EGGDLIVVI 1139

RESULT 32
Q99ZL6
ID Q99ZL6 PRELIMINARY; PRT; 116 AA.
AC Q99ZL6;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Putative methylmalonyl-CoA decarboxylase, gamma-subunit (EC 4.1.1.41).
DE (EC 4.1.1.41).
GN SPY1176.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SF370 / ATCC 700294 / Serotype M1;
RX MEDLINE=21192684; PubMed=11296296;
RA Ferretti J.J., McShan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K., Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P., Qian Y., Jia H.G., Najjar F.Z., Ren Q., Zhu H., Song L., White J., Yuan X., Clifton S.W., Roe B.A., McLaughlin R.;
RA "Complete genome sequence of an M1 strain of Streptococcus pyogenes.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).
CC -!- COFACTOR: BIOTIN (BY SIMILARITY).
DR EMBL; AE006558; AAK34043.1; -.
DR HSSP; P02905; 1BDO.
DR GO; GO:0009374; F:biotin binding; IEA.
DR GO; GO:0016829; F:lyase activity; IEA.
DR GO; GO:0004492; F:methylmalonyl-CoA decarboxylase activity; IEA.
DR InterPro; IPR001882; Biotin_BS.
DR InterPro; IPR000089; Biotin_lipoyl.
DR Pfam; PF00364; biotin_lipoyl; 1.
DR PROSITE; PS00188; BIOTIN; 1.
KW Biotin; Lyase; Complete proteome.
SQ SEQUENCE 116 AA; 12288 MW; A245219AC595BFEC CRC64;

Query Match 45.6%; Score 156; DB 16; Length 116;
Best Local Similarity 52.3%; Pred. No. 1.2e-08;
Matches 34; Conservative 7; Mismatches 24; Indels 0; Gaps 0;

QY 3 EIPAPLAGTVSKILVKEGDTVKGQTVLVLEAMKMETEINAPTDGKVEKVLVKERDAVQG 62
Db 50 QVKAPMSGTVLSIFATEGKAVKGEAVLVLEAMKMEINELAPADGLVSKIHVVANQTVES 109
QY 63 QGGLI 67
Db 110 EQVLI 114
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Matches 34; Conservative 7; Mismatches 24; Indels 0; Gaps 0;	
QY	3 EIPAPLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVLVXKRDVQ 62
Db	50 QVKAPMSGTVLSIFATEGKAVKGEAVLVLEAMKMENEILAPADGLVSKIHVVANQMVES 109
QY	63 GQGLI 67
Db	110 EQVLI 114
RESULT 38	
Q8RAJ2	
ID	Q8RAJ2 PRELIMINARY; PRT; 135 AA.
AC	Q8RAJ2;
DT	01-JUN-2002 (TREMBlrel. 21, Created)
DT	01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DT	01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE	Biotin carboxyl carrier protein.
GN	ACCB OR TTE1222.
OS	Thermoanaerobacter tengcongensis.
OC	Bacteria; Firmicutes; Clostridia; Thermoanaerobacteriales;
OC	Thermoanaerobacteriaceae; Thermoanaerobacter.
OX	NCBI_TaxID=119072;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=MB4 / JCM 11007;
RX	MEDLINE=21992816; PubMed=11997336;
RA	Bao Q., Tian Y., Li W., Xu Z., Xuan Z., Hu S., Dong W., Yang J.,
RA	Chen Y., Xue Y., Xu Y., Lai X., Huang L., Dong X., Ma Y., Ling L.,
RA	Tan H., Chen R., Wang J., Yu J., Yang H.;
RT	"A complete sequence of T. tengcongensis genome.";
RL	Genome Res. 12:689-700(2002).
DR	EMBL; AE013084; AAM24452.1; -.
DR	GO; GO:0009374; F:biotin binding; IEA.
DR	InterPro; IPR001882; Biotin_BS.
DR	InterPro; IPR000089; Biotin_lipoyl.
DR	Pfam; PF00364; biotin_lipoyl; 1.
DR	PROSITE; PS00188; BIOTIN; 1.
KW	Complete proteome.
SQ	SEQUENCE 135 AA; 15195 MW; 9C2BF717C008800A CRC64;
Query Match 44.7%; Score 153; DB 16; Length 135;	
Best Local Similarity 47.8%; Pred. No. 2.9e-08;	
Matches 33; Conservative 11; Mismatches 23; Indels 2; Gaps 1;	
QY	1 EGE--IPAPLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVLVXKRD 58
Db	64 EGEKTTAPMPGTIVDVRVKEGDKVKRGDVIVILEAMKMENEIMAPENGTVSVNVAKGD 123
QY	59 AVQGGQGLI 67
Db	124 TVNRGDIIV 132
RESULT 39	
O67544	
ID	O67544 PRELIMINARY; PRT; 620 AA.
AC	O67544;
DT	01-AUG-1998 (TREMBlrel. 07, Created)
DT	01-AUG-1998 (TREMBlrel. 07, Last sequence update)
DT	01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE	Oxaloacetate decarboxylase alpha chain.
GN	OADA OR AQ 1614.
OS	Aquifex aeolicus.
OC	Bacteria; Aquificae; Aquificales; Aquificaceae; Aquifex.
OX	NCBI_TaxID=63363;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=VF5;
RX	MEDLINE=98196666; PubMed=9537320;
RA	Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,
RA	Graham D.E., Overbeek R., Snead M.A., Keller M., Aujaay M., Huber R.,
Query Match 44.4%; Score 152; DB 1; Length 167;	
Best Local Similarity 50.7%; Pred. No. 4.7e-08;	
Matches 34; Conservative 9; Mismatches 24; Indels 0; Gaps 0;	
RA	Feldman R.A., Short J.M., Olson G.J., Swanson R.V.;
RT	"The complete genome of the hyperthermophilic bacterium Aquifex
RT	aeolicus.";
RL	Nature 392:353-358(1998).
DR	EMBL; AE000747; AAC07497.1; -.
DR	PIR; F70439; F70439.
DR	HSSP; P02905; 1BDO.
DR	GO; GO:0005874; C:microtubule; IEA.
DR	GO; GO:0009374; F:biotin binding; IEA.
DR	GO; GO:0003824; F:catalytic activity; IEA.
DR	GO; GO:0005525; F:GTP binding; IEA.
DR	GO; GO:0008948; F:oxaloacetate decarboxylase activity; IEA.
DR	GO; GO:0005198; F:structural molecule movement; IEA.
DR	GO; GO:0007018; P:microtubule-based movement; IEA.
DR	GO; GO:0006814; P:sodium ion transport; IEA.
DR	InterPro; IPR002453; Beta tubulin.
DR	InterPro; IPR001882; Biotin_BS.
DR	InterPro; IPR000089; Biotin_lipoyl.
DR	InterPro; IPR000891; HMGL-like.
DR	InterPro; IPR005776; Oada.
DR	InterPro; IPR003379; PYC OADA.
DR	Pfam; PF00364; biotin_lipoyl; 1.
DR	Pfam; PF00682; HMGL-like; 1.
DR	Pfam; PF02436; PYC OADA; 1.
DR	TIGRFAMS; TIGR01108; oada; 1.
DR	PROSITE; PS00188; BIOTIN; 1.
DR	PROSITE; PS00228; TUBULIN_B_AUTOREG; 1.
KW	Complete proteome.
SQ	SEQUENCE 620 AA; 70416 MW; 4F306D48794AE859 CRC64;
Query Match 44.7%; Score 153; DB 16; Length 620;	
Best Local Similarity 45.6%; Pred. No. 1.6e-07;	
Matches 31; Conservative 14; Mismatches 23; Indels 0; Gaps 0;	
QY	2 GEIPAPLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVLVXKRDVQ 61
Db	545 GDVTSPTITGKVNINIKVNVGDEVKEGDVLLVVEAMKMENIHSFVDFVIVRGETVN 604
QY	62 GQGLIKI 69
Db	605 PDEVLIIRI 612
RESULT 40	
O52603	
ID	O52603 PRELIMINARY; PRT; 167 AA.
AC	O52603;
DT	01-JUN-1998 (TREMBlrel. 06, Created)
DT	01-JUN-1998 (TREMBlrel. 06, Last sequence update)
DT	01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE	Biotin carboxyl carrier protein.
GN	ACCB.
OS	Sulfolobus metallicus.
OC	Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
OC	Sulfolobus.
OX	NCBI_TaxID=47303;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=LM;
RX	MEDLINE=20059326; PubMed=10591844;
RA	Burton N.P., Williams T.D., Norris P.R.;
RT	"Carboxylase genes of Sulfolobus metallicus.";
RL	Arch. Microbiol. 172:349-353(1999).
DR	EMBL; AF042099; AAB97085.1; -.
DR	PIR; T44291; T44291.
DR	HSSP; P02905; 1BDO.
DR	InterPro; IPR000089; Biotin_lipoyl.
DR	Pfam; PF00364; biotin_lipoyl; 1.
SQ	SEQUENCE 167 AA; 18580 MW; F05A04F38BC55B09 CRC64;

